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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:31:17 ; Search time 217 Seconds
(without alignments)
5815.985 Million cell updates/sec

Title: US-09-493-601B-1

Perfect score: 710

Sequence: 1 atgtcgggcaataacatgtc.....tgacgtcactaagagcctt 710

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708.4	99.8	1486	2	US-09-022-940-4
2	708.4	99.8	1486	3	US-09-216-386-4
3	708.4	99.8	1556	3	US-09-629-645A-18
4	708.4	99.8	2417	3	US-09-629-645A-3
5	667.2	94.0	2421	3	US-09-949-016-4023
6	667.2	94.0	6421	3	US-09-949-016-15765
7	667.2	94.0	14126	3	US-09-949-016-15171
8	565	79.6	693	3	US-09-629-645A-10
9	556.4	78.4	777	3	US-09-629-645A-21
10	552.8	77.9	709	2	US-08-844-120-2
11	552.8	77.9	709	3	US-09-022-940-2
12	552.8	77.9	709	3	US-09-216-386-2
13	552.8	77.9	709	3	US-09-213-394-2
14	552.8	77.9	709	3	US-09-988-982-2
15	500	70.4	601	3	US-09-949-016-12098
16	500	70.4	601	3	US-09-949-016-14287
17	313.6	44.2	601	3	US-09-949-016-12099
18	313.6	44.2	601	3	US-09-949-016-12209
19	277.6	39.1	1624	3	US-09-013-881-15
20	277.6	39.1	1624	3	US-09-612-473-15
21	249.2	35.1	601	3	US-09-949-016-14288
22	212	29.9	457	3	US-09-621-976-2471
23	176.8	24.9	601	3	US-09-949-016-14289
24	172.4	24.3	559	3	US-09-612-473-49

25	156.8	22.1	601	3	US-09-949-016-142290	Sequence 142290,
26	99.6	14.0	608	3	US-09-629-645A-20	Sequence 20, Appl
27	75	10.6	675	3	US-09-540-236-1521	Sequence 1521, Ap
28	71.8	10.1	62909	3	US-09-596-002-32	Sequence 32, Appl
29	69.2	9.7	975	3	US-09-216-001-2	Sequence 2, Appli
30	69.2	9.7	975	3	US-08-878-862-2	Sequence 2, Appli
31	68.2	9.6	852	3	US-09-599-360B-9	Sequence 9, Appli
32	68.2	9.6	852	3	US-09-599-360B-61	Sequence 61, Appl
33	68.2	9.6	852	3	US-09-513-999C-9	Sequence 9, Appli
34	68.2	9.6	852	3	US-09-471-276-9	Sequence 9, Appli
35	65.6	9.2	774	3	US-09-248-796A-1951	Sequence 1951, Ap
36	60.8	8.6	466	3	US-09-612-473-50	Sequence 50, Appl
37	60.8	8.6	67181	3	US-09-949-016-13102	Sequence 13102, A
38	58.2	8.2	545	3	US-09-533-559-5020	Sequence 5020, Ap
39	53	7.5	260	3	US-09-612-473-48	Sequence 48, Appl
40	45.6	6.4	777	3	US-09-252-991A-3689	Sequence 3689, Ap
41	41.4	5.8	278	3	US-09-313-294A-3545	Sequence 3545, Ap
42	41.2	5.8	255	3	US-09-248-796A-1952	Sequence 1952, Ap
43	40	5.6	260247	3	US-09-949-016-13358	Sequence 13358, A
44	39.4	5.5	601	3	US-09-949-016-112652	Sequence 112652,
45	39.4	5.5	1732	3	US-09-023-655-741	Sequence 741, App

ALIGNMENTS

RESULT 1
US-09-022-940-4
; Sequence 4, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1486 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-022-940-4

Query Match 99.8%; Score 708.4; DB 2; Length 1486;
Best Local Similarity 99.9%; Pred. No. 6.1e-234;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1	ATGTGGGGCAATAACTGTCAACCCGGTCCCGCCGATCTGTCCGCGCCGCGGAAGGCC	60
76	ATGTGGCGCAATAACATGTCAACCCGGTCCCGCCGATCTGTCCGCGCCGCGGAAGGCC	135
61	ACCGCTGGCGTGATTTTCTCGATGGATTGGGAGTACTGGGCACGGATGGGCAGAAGCC	120
136	ACCGCTGGCGTGATTTTCTCGATGGATTGGGAGTACTGGGCACGGATGGGCAGAAGCC	195
121	TTTGGCAGGTATCAGAAGTTTCATATCAAATATATCTGCCCGCATGGGCGCTGTAGGCCT	180
196	TTTGGCAGGTATCAGAAGTTTCATATCAAATATATCTGCCCGCATGGGCGCTGTAGGCCT	255
181	GTTTCACTAAATATGAAACGTGGCTATGCTTCATGGTTTGATATATTTGGGCTTTCACCA	240
256	GTTTCACTAAATATGAAACGTGGCTATGCTTCATGGTTTGATATATTTGGGCTTTCACCA	315
241	GATTCACAGGAGGATGAATCTGGGATTAACACGACGACGAGAAATATATAAGCTTTGATT	300
316	GATTCACAGGAGGATGAATCTGGGATTAACACGACGACGAGAAATATATAAGCTTTGATT	375
301	GATCAAGAAGTCAAGATGGCAATTCCTTCTTAACAGAAATATTTTGGAGGGTTTCTCTAG	360
376	GATCAAGAAGTCAAGATGGCAATTCCTTCTTAACAGAAATATTTTGGAGGGTTTCTCTAG	435
361	GGAGGAGCTTTTATCTTTATATACTGCCCTTACCACACAGCAGAGAACTGGCAGGTGTCACT	420
436	GGAGGAGCTTTTATCTTTATATACTGCCCTTACCACACAGCAGAGAACTGGCAGGTGTCACT	495
421	GCACCTAGTTGTGGCGTTCCACTTTCGGGGCTCCCTTCCACAGGGTCTATCGGTGGTGTCT	480
496	GCACCTAGTTGTGGCGTTCCACTTTCGGGGCTCCCTTCCACAGGGTCTATCGGTGGTGTCT	555
481	AATAGAGATATTTCTATTCTCCAGTGGCCACGGGGAATGTGACCCCTTTGGTTCCCTCTGATG	540
556	AATAGAGATATTTCTATTCTCCAGTGGCCACGGGGAATGTGACCCCTTTGGTTCCCTCTGATG	615
541	TTTGGTCTCTTTACGGTGGAAAAAATAAAAAATTCAGCCAAATGTGACCTTT	600
616	TTTGGTCTCTTTACGGTGGAAAAAATAAAAAATTCAGCCAAATGTGACCTTT	675
601	AAAACTTATGAAGGTATGATGCACAGTTTCGTGTCTCAACAGGAAATGATGGATGTCAAGCAA	660
676	AAAACTTATGAAGGTATGATGCACAGTTTCGTGTCTCAACAGGAAATGATGGATGTCAAGCAA	735
661	TTTATTGATAAACTCTCACTCCATTGATTGACGTCACTAAGAGGCGCTT	710
736	TTTATTGATAAACTCTCACTCCATTGATTGACGTCACTAAGAGGCGCTT	785

RESULT 2

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US-09-216-386-4
; Sequence 4, Application US/09216386
;
; Patent No. 6093561
;
; GENERAL INFORMATION:
;
; APPLICANT: Hillman, Jennifer L.
;
; APPLICANT: Shah, Purvi
;
; APPLICANT: Murry, Lynn E.
;
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
;
; NUMBER OF SEQUENCES: 5
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSSEE: Incyte Pharmaceuticals, Inc.
;
; STREET: 3174 Porter Dr.
;
; CITY: Palo Alto
;
; STATE: CA
;
; COUNTRY: USA
;
; ZIP: 94304
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
;
; OPERATING SYSTEM: DOS
;
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/216.386
;

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	FILING DATE:	PRIOR APPLICATION DATA:	09/022,940	
	APPLICATION NUMBER:	09/022,940		
	FILING DATE:			
	ATTORNEY/AGENT INFORMATION:			
	NAME: Billings, Lucy J.			
	REGISTRATION NUMBER: 36,749			
	REFERENCE/DOCKET NUMBER: PF-0269-1 CIP			
	TELECOMMUNICATION INFORMATION:			
	TELEPHONE: 650-855-0555			
	TELEFAX: 650-845-4166			
	INFORMATION FOR SEQ ID NO: 4:			
	SEQUENCE CHARACTERISTICS:			
	LENGTH: 1486 base pairs			
	TYPE: nucleic acid			
	STRANDEDNESS: single			
	TOPOLOGY: linear			
	US-09-216-386-4			
	Query Match	99.8%; Score 708.4; DB 3; Length 1486;		
	Best Local Similarity	99.9%; Pred. No. 6.1e-334;		
	Matches	709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1	ATGTGGCGCAATAACATGTCACCCCGCTGCCCGCATCGTGC CGCGCAGGAGGCC 60		
Dd	76	ATGTGGCGCAATAACATGTCACCCCGCTGCCCGCATCGTGC CGCGCAGGAGGCC 135		
Qy	61	ACCCTCGCGTGATTTTCTCGCATGGAATGGGAGATATCGGGCACGSATGGGAGAACGCC 120		
Dd	136	ACCCTCGCGTGATTTTCTCGCATGGAATGGGAGATATCGGGCACGSATGGGAGAACGCC 195		
Qy	121	TTTGCAGGTATCAGAAGTTCCATATCAAATATATCTGCCCGCATCGCGCTGTTAGCCCT 180		
Dd	196	TTTGCAGGTATCAGAAGTTCCATATCAAATATATCTGCCCGCATCGCGCTGTTAGCCCT 255		
Qy	181	GTTACATTAATATGAACGTGGCTATGCCCTTCATGGTTTCATATATTGGCTTTTCACCA 240		
Dd	256	GTTACATTAATATGAACGTGGCTATGCCCTTCATGGTTTCATATATTGGCTTTTCACCA 315		
Qy	241	GATTTCACAGGAGATGAATCTGGGATTTAAACAGGCAGCAGAAAAATATAAAGCTTTGATT 300		
Dd	316	GATTTCACAGGAGATGAATCTGGGATTTAAACAGGCAGCAGAAAAATATAAAGCTTTGATT 375		
Qy	301	GATCAAGAAGTAGAATAGGCAATCCCTTTCAAACAATATATTTCGGAGGGTTTTCTCAG 360		
Dd	376	GATCAAGAAGTAGAATAGGCAATCCCTTTCAAACAATATATTTCGGAGGGTTTTCTCAG 435		
Qy	361	GGAGGACTTTATCTTTATATATCTGCCCTTACACACAGCAGAAAATCTGGCAGGTGTCACT 420		
Dd	436	GGAGGACTTTATCTTTATATATCTGCCCTTACACACAGCAGAAAATCTGGCAGGTGTCACT 495		
Qy	421	GCACCTCAGTTGCTGGCTTCCAATCTCGGGCTTCCTTTCCACAGGGTCTCATTCGGTGGTCT 480		
Dd	496	GCACCTCAGTTGCTGGCTTCCAATCTCGGGCTTCCTTTCCACAGGGTCTCATTCGGTGGTCT 555		
Qy	481	AATAGAGATATTTCTATPTTCCAGTGCCACGGGATTTGTGACCCCTTGGTTCCCCTGATG 540		
Dd	556	AATAGAGATATTTCTATPTTCCAGTGCCACGGGATTTGTGACCCCTTGGTTCCCCTGATG 615		
Qy	541	TTTGGTTCTCTTACGGTGGAAAACCTA AAAACATTTGGTGAATCCAGCCAATGTCAACCTTT 600		
Dd	616	TTTGGTTCTCTTACGGTGGAAAACCTA AAAACATTTGGTGAATCCAGCCAATGTCAACCTTT 675		
Qy	601	AAAACCTATCAAGGTATGATGCACAGTTTCGTTGTCAAACAGGAAATGATGGATGTCAAGCAA 660		
Dd	676	AAAACCTATCAAGGTATGATGCACAGTTTCGTTGTCAAACAGGAAATGATGGATGTCAAGCAA 735		
Qy	661	TTCATTGATAAATCTCTTACCTTCCAAATTTGATTGACGTCACTAAGAGGCCTT 710		
Dd	736	TTCATTGATAAATCTCTTACCTTCCAAATTTGATTGACGTCACTAAGAGGCCTT 785		

RESULT 3

```
US-09-629-645A-18
; Sequence 18, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 18
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (195)...(887)
US-09-629-645A-18

Query Match          99.8%; Score 708.4; DB 3; Length 1556;
Best Local Similarity 99.9%; Pred. No. 6.3e-234;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCATCAACCCCGCTGCGCGCCATCGTCCCGCCCGCCGGAAGGCC 60
DB 195 ATGTGCGGCAATAAATGTCATCAACCCCGCTGCGCGCCATCGTCCCGCCCGCCGGAAGGCC 254
QY 61 ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTGGGACGATGCGGACGAAGCC 120
DB 255 ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTGGGACGATGCGGACGAAGCC 314
QY 121 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
DB 315 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 374
QY 181 GTTACATTAATAATGAAGTGGCTATGCTTCAATGTTTGAATATTTGGGCTTTTCAACA 240
DB 375 GTTACATTAATAATGAAGTGGCTATGCTTCAATGTTTGAATATTTGGGCTTTTCAACA 434
QY 241 GATTCACAGGAGTGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 300
DB 435 GATTCACAGGAGTGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 494
QY 301 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGGAGGTTTCTCAG 360
DB 495 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGGAGGTTTCTCAG 554
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCTTACACACAGCAAACTGGCAGGTGTCAT 420
DB 555 GGAGGAGCTTTATCTTTTATATATCTGCTTACACACAGCAAACTGGCAGGTGTCAT 614
QY 421 GCATCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 480
DB 615 GCATCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 674
QY 481 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTTGGTCCCTTGATG 540
DB 675 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTTGGTCCCTTGATG 734
QY 541 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 735 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTTGGTGAATCCAGCCAAATGTGACCTTT 794
QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAATGATGATGTCAGCA 660
DB 795 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAATGATGATGTCAGCA 854
QY 661 TTTCATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACCTAAGAGGCTTT 710
DB 855 TTTCATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACCTAAGAGGCTTT 904
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US-09-629-645A-3
; Sequence 3, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 3
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(728)
US-09-629-645A-3

Query Match          99.8%; Score 708.4; DB 3; Length 2417;
Best Local Similarity 99.9%; Pred. No. 8.6e-234;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCATCAACCCCGCTGCGCGCCATCGTCCCGCCCGCCGGAAGGCC 60
DB 36 ATGTGCGGCAATAAATGTCATCAACCCCGCTGCGCGCCATCGTCCCGCCCGCCGGAAGGCC 95
QY 61 ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTGGGACGATGCGGACGAAGCC 120
DB 96 ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTGGGACGATGCGGACGAAGCC 155
QY 121 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
DB 156 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 215
QY 181 GTTACATTAATAATGAAGTGGCTATGCTTCAATGTTTGAATATTTGGGCTTTTCAACA 240
DB 216 GTTACATTAATAATGAAGTGGCTATGCTTCAATGTTTGAATATTTGGGCTTTTCAACA 275
QY 241 GATTCACAGGAGTGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 300
DB 276 GATTCACAGGAGTGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 335
QY 301 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGGAGGTTTCTCAG 360
DB 336 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGGAGGTTTCTCAG 395
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCTTACACACAGCAAACTGGCAGGTGTCAT 420
DB 396 GGAGGAGCTTTATCTTTTATATATCTGCTTACACACAGCAAACTGGCAGGTGTCAT 455
QY 421 GCATCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 480
DB 456 GCATCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 515
QY 481 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTTGGTCCCTTGATG 540
DB 516 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTTGGTCCCTTGATG 575
QY 541 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 576 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTTGGTGAATCCAGCCAAATGTGACCTTT 635
QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAATGATGATGTCAGCA 660
DB 636 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAATGATGATGTCAGCA 695
QY 661 TTTCATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACCTAAGAGGCTTT 710
DB 696 TTTCATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACCTAAGAGGCTTT 745
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Db	2576	GTTTGGTTCTCTTAAGGTTGAAAAA	CAATTGGTGAATCCAGCAATGTGACCT	2635	
Qy	599	TTAAAACTATGAAGGTATGATGAC	AGTTCGGTGTCAA	CGAGAAATGATGTGTAACG	658
Db	2636	TTAAACCTCTGAAGGTTATGATGAC	ACAGTTCGGTGTCAA	CGAGAAATGATGTGTAACG	2695
Qy	659	AAATCATTTGATAAACTCTCACT	CCCAATTGATTTGACGTCACT	TAAGAGGCCCTT	710
Db	2696	AAATCATTTGATAAACTCTCACT	CCCAATTGATTTGACGTCACT	TAAGAGGCCCTT	2747

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RESULT 7
US-09-949-016-15171/c
; Sequence 15171, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15171
; LENGTH: 14126
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15171

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Query Match	94.08;	Score 667.2;	DB 3;	Length 14126;
Best Local Similarity	97.99;	Pred. No. 5.3e-219;		
Matches 697;	Conservative 0;	Mismatches 13;	Indels 2;	Gaps 2;
Qy	1	ATGTGGCGCAATAACATGTGTAACCCCGCTGCGCCGCACTCGTGCCGCGCGCCCGAAGGCC	60	
Db	2735	ATGTGGCGCAATAACATGTCAACCCCGCTGCCCACTGTCGTCGCGCGCGCCCGAAGGCC	2676	
Qy	61	ACCCTCGCGTGAATTTTCTCGATGGATGGAGATACTGGCACGGATGGGCAGAAAGCC	120	
Db	2675	ACCACTGAGGTGAATTTTCTCGATGGATGGAGATACTGGCACGGATGGGCAGAAAGCC	2616	
Qy	121	TTTGCAGGTATCAGAAGTTACATATCAAAATATATCTGCCCGCATGCGCCTGTAGGCCT	180	
Db	2615	TTTGCAGGTATCAGAAGTTCACATATCAAAATATATCTGCCCGCATGCGCCTGTAGGCCT	2556	
Qy	181	GTT-ACATTAATATGAACGTGGCTATGCGCTTCATGGTTTGATATTATTTGGGCTTTCCACC	239	
Db	2555	GTTAAACATTAATATGAACATAGTATGCGCTTCATGGTTTGATATTATTTGGGCTTTCCACC	2496	
Qy	240	AGATTTCACAGGAGGATGAATCTGGGATTTAAACAGGCAGCAGAAATATAAAAGCTTTTGAT	299	
Db	2495	AGATTTCACAGGAGGATGAATCTGGGATTTAAACAGGCAGCAGAAATATAAAAGCTTTTGAT	2436	
Qy	300	TGATCAAGAAGTGAAGAATGGCATTCCTTCTTAAACAGAAATTATTTTGGGAGGGTTTCTCA	359	
Db	2435	TGATCAAGAAGTGAAGAATGGCATTCCTTCTTAAACAGAAATTATTTTGGGAGGGTTTCTCA	2376	
Qy	360	GGGAGGAGCTTTATCTTTTATATATGCGCCTTACCACACAGCAGAAACTGGCAGGTGTCAC	419	
Db	2375	GGGAGGAGCTTTATCTTTTATATATGCGCCTTACCACACAGCAGAAACTGGCAGGTGTCAC	2316	
Qy	420	TGCACTCAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGGTCTCTATCGGTGGTGC	479	
Db	2315	TGCACTCAATTCGTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGGTCTCTATCGGTGGTGC	2256	
Qy	480	TAATAGAGATATTTCTATTTCTCCAGTGCACGGGATTTGTGACCCCTTTGGTTCCCTCGAT	539	

Db	2255	TAATAGAGATATTTCTATTCTCCAGTGCACGGGGATTGTGACCCCTTGGTCCCTCCCTGAT	2196
Qy	540	GTTTGGTTCCTTACCGGTGGAAAAACT-AAAAACATTGGTGAATCAGGCCAATGTGACCT	598
Db	2195	GTTTGGTTCCTTACCGGTGAAAAACTAAAAACATTGGTGAATCAGGCCAATGTGACCT	2136
Qy	599	TTAAAACTTATGAAGGTATGATGCACAGTTCGTGTCAAAGGAAATGATGGATGTCAAAGC	658
Db	2135	TTAAAACTTATGAAGGTATGATGCACAGTTCGTGTCAAAGGAAATGATGAATGTCAAAGC	2076
Qy	659	AATTCATTGATAAACTCCTACCTCCAAATTGATTGACGTCACTAAGAGGCCCTT	710
Db	2075	AATTCATTGATAAACTCCTACCTCCAAATTGATTGAGCTCACTAAGAGGCCCTT	2024

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RESULT 8
US-09-629-645A-10
; Sequence 10, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 10
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(693)
US-09-629-645A-10

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Query Match	79.6%	Score 565	DB 3	Length 693
Best Local Similarity	88.5%	Pred. No. 1.5e-184		
Matches 613	Conservative 0	Mismatches 80	Indels 0	Gaps 0
Qy	1	ATGTGGCGCAATACATGTCAACCCCGCTGCCCGCCGATCTGTGCCGCGCCCGAAGGCC	60	
Db	1	ATGTGGCGCAACACATGTCCGCTCCGATGCCCGCGCTGTGTCCGCGCCCGCCGGAAGGCC	60	
Qy	61	ACGCTCGCGTGAATTTTCTTGCACTGATTTGGAGATACTGGGCACGATGGGCAGAAAGCC	120	
Db	61	ACGCCCGCGTATTTTCTTTCACGATTTGGAGATACAGGGCATGATGGGCAGAAAGCC	120	
Qy	121	TTTTCAGGATATCAGAAGTTCCATATATCAAAATATATCTGCCCGATCGCCTGTGAGCGCT	180	
Db	121	TTTTCAGGATCAAAAGTCCCAATCAATATCATCTGTCCACATGCCCTGTGATGCCA	180	
Qy	181	GTTACATTAATATGAAGTGGGTATGCGTTTCATGHTTTCATATATTGGCTTTTCACCA	240	
Db	181	GTCACTTAATATGAATATGGCTATGCGTTTCATGHTTTCATATCGTTGGACTTTTCACCA	240	
Qy	241	GATTCACAGGAGTGAATCTGGGATTAACACGCGCAGCAAAAATATAAAGCTTTTCATT	300	
Db	241	GATTTCCAGGAGATGAATCTGGAAATTAACACGCGCAGCAAAACCGTTAAAGCCTTGATA	300	
Qy	301	GATCAAGAAGTGAAGAATGGCATTCCTTTCTAAACAGAAATATATTTGGGAGGGTTTTCTCAG	360	
Db	301	GATCAAGAAGTGAAGAATGSCATTCCTTTCTAAACAGGATATATTTGGGAGGATTTTTCTCAG	360	
Qy	361	GGAGGAGCTTTATCTTTTATATATCGCCCTTACCAACAGCAGAAACTGGCAGGTGTCACT	420	
Db	361	GGAGGCGCTTGTCTTTTATACACTGCTCTCACACACAGCAGAAACTGGGTGGTGTCACT	420	
Qy	421	GCACTCAGTTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGCTCTATTCGGTGTGCT	480	
Db	421	GCACTCAGTTGCTGGCTTCCACTTTGGGCTTCTGTTTTACAGGGGCGCATCAACAGTGTCT	480	

QY 481 AATAGAGATATTCTTATCTCCAGTCCACCGGGATTTGTGACCTTTTGGTTCCTCCCTGATG 540
DB AATAGAGATATTCTTATCTCCAGTCCACCGGGATTTGTGACCTTTTGGTTCCTCCCTGATG 540
QY 541 TTTGGTCTCTTACCGTGGAAACCTAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
DB TTTGGTCTCTTACCGTGGAAACCTAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTCTCAACAGGAATGATGGATGTCAAGCAA 660
DB AAAACCTATGAAGGTATGATGACACAGTTCGTCTCAACAGGAATGATGGATGTCAAGCAA 660
QY 661 TTTATTGATAAACTCTTACCTCCAATTTGATCA 693
DB TTTATTGATAAACTCTTACCTCCAATTTGATCA 693

RESULT 9

US-09-629-645A-21
; Sequence 21, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 21
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 639
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 684
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 712
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 719
; OTHER INFORMATION: unknown
; NAME/KEY: CDS
; LOCATION: (38)...(727)

US-09-629-645A-21

Query Match 78.4%; Score 556.4; DB 3; Length 727;
Best Local Similarity 87.7%; Pred. No. 1.5e-181;
Matches 605; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 1 ATGTGGCGCAATAACATGTCAACCCCGTCCCGCCATCGTCCCGCCCGCCCGCGAAGGCC 60
DB 38 ATGTGGCGCAACAAATGTCCTCGATGCCCGCGTGTGCGCGCCCGCCCGAAGGCC 97
QY 61 ACCGCTCGGGTGATTTCTCTGATGATTTGGAGATATCTGGGACGATGGGACAGAGCC 120
DB 98 ACCGCGGGGTTATTTCTTCAACGATTTGGAGATACAGGCGATGATGGGACAGAGCC 157
QY 121 TTTGAGGTATCAGAAATTCATATCAATATATCTGCCCGATGCGGCTGTAGGCTT 180
DB 158 TTTGAGGTATCAGAAATTCATATCAATATATCTGCCCGATGCGGCTGTAGGCTT 217
QY 181 GTTACATTAATATGAAGTGGCTATGCTTCAATGTTTGTATTTATTTGGGCTTTTCAACA 240
DB 218 GTTACATTAATATGAATGCTATGCTTCTTGGTTGATATCGTTGACATTTTCAACA 277
QY 241 GATTCACGAGGATGAATCTCGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300
DB 278 GATTCACGAGGATGAATCTCGGATTAACAGGACAGAGAAATATAAAGCTTTGATA 337

QY 301 GATCAAGAAGTGAAGAATGGCATTCCTTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB GATCAAGAAGTGAAGAATGGCATTCCTTCTTAACAGAAATATTTTGGAGGATTTTCTCAG 397
QY 361 GGAGAGCTTTATCTTTTATATACTGCCCTTACCACACAGCAGAAATGTCAGGTGTCAC 420
DB GGAGGCGCTTGTCTTTTATACACTGCTCTCACACACAGCAGAAATGTCAGGTGTCAC 457
QY 421 GCACCTCAGTCTGCGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGTGCT 480
DB GCACCTCAGTCTGCGGCTTCCACTTCGGGCTTCCCTTCCACAGGGGCGGATCAACAGTGT 517
QY 481 AATAGAGATATTCTTATCTCCAGTCCACCGGGATTTGTGACCTTTTGGTTCCTCCCTGATG 540
DB AATAGAGATATTCTTATCTCCAGTCCACCGGGATTTGTGACCTTTTGGTTCCTCCCTGATG 577
QY 541 TTTGGTCTCTTACCGTGGAAACCTAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
DB TTTGGTCTCTTACCGTGGAAACCTAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 637
QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTCTCAACAGGAATGATGGATGTCAAGCAA 660
DB AAAACCTATGAAGGTATGATGACACAGTTCGTCTCAACAGGAATGATGGATGTCAAGCAA 697
QY 661 TTTATTGATAAACTCTTACCTCCAATTTGAT 690
DB TTTATTGATAAACTCTTACCTCCAATTTGAT 727

RESULT 10

US-08-844-120-2
; Sequence 2, Application US/08844120
; Patent No. 5858756
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT19
; CLONE: 2676650
US-08-844-120-2

Db 669 TTCATTGATAAACTCCTACCTCCAATTGATTGACGTCACCTA 709

RESULT 12

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US-09-216-386-2
; Sequence 2, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASCSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386

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Query Match 77.9%: Score 552.8: DB 3: Length 709:

Query Match 77.9%; Score 552.8; DB 3;
Best [ocal Similarity 89.9%; Pred. No. 2.5e-180;

Best Local Similarity	89.9%	Pred: No. 2.5e-180;	
Matches	630:	Conservative	1:
Mismatches	630:	Indels	4:
Gaps	66:		

[illegible]

361	Qy	GGAGGACCTTTATCTTTTATATATATCTGCGCTTACCA	CACAGCAGAGAAACTGGCAGGTGTCACT	421
369	Db	GGAGGACCTTTATCTTTTATATATCTGCGCTTACCA	CACAGCAGAACTGGCAGGTGTCACT	428
421	Qy	GCACCTAGTTCGTGGCTTCCACTTTCGGGCTTCCCT	TTCCACAGGGTCCCTATCGGTGGTGCT	480
429	Db	GCACCTAGTTCGTTCGTTCCTTTCGGGNTTCCT	TTCCACAGGGKCCCTATCGGTGGTGCT	488
481	Qy	AATAGAGATATTTCTATTCTCCAGTGCCACGGGGAT	TGTGACCCCTTTGGTTCCTCCCTGATG	540
489	Db	AATAGAGATATTTCTATTCTCCAGTGCCACGGGGAT	TGTGACCCCTTTGGTTCCTCCCTGATG	548
541	Qy	TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTTGGT	GAAATCCAGCCAAATGTGACCTTTT	600
549	Db	TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTTGGT	GAAATCCAGCCAAATGTGACCTTTT	608
601	Qy	AAAACTTATGAAGTATGATGCA	CAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA	660
609	Db	AAAACTTATGAAGTATGATGCA	CAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA	668
661	Qy	TTCAATTGATAAACTCCTACCTCCAAATTGATTCAGTCACTA		701
669	Db	TTCAATTGATAAACTCCTACCTCCAAATTGATTCAGTCACTA		709

RESULT 13

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US-09-213-394-2
; Sequence 2, Application US/09213394
; Patent No. 6319701
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,394
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT19
; CLONE: 2676650
US-09-213-394-2

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Query Match 77.9%; Score 552.8; DB 3; Length 709;

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Best Local Similarity 89.9%; Pred. No. 2.5e-180;
Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;

QY 1 ATGTGGCGCAATAAATGATCAACCCCGCTGCCCGCATCGTGCCTCCGCGCCGCGGAGGCC 60
Db 75 ATGTGGCGCAATAAATGATCAACCCCGCTGCCCGCATCGTGCCTCCGCGCCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTTCTGCAATGATGGGAGATACCTGGGACCGATGGGAGGCC 120
Db 135 ACCGCTGCGGTGATTTTCTGCAATGATGGGAGATACCTGGGAGGCC 175
QY 121 TTTGCAGGTATCAGAAGTTACATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
Db 176 -----GCTGTAGGCT 188
QY 181 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCAACA 240
Db 189 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCAACA 248
QY 241 GATTACAGGAGGATGAATCTGGGATTAACACGCGACGAGAAATATAAAGCTTTGATT 300
Db 249 GATTACAGGAGGATGAATCTGGGATTAACACGCGACGAGAAATATAAAGCTTTGATT 308
QY 301 GATCAAGAGTGAAGATGCGATTCCTTCTAAGAAATATTTTGGAGGGTTTCTCAG 360
Db 309 GATCAAGAGTGAAGATGCGATTCCTTCTAAGAAATATTTTGGAGGGTTTCTCAG 368
QY 361 GGAGGAGCTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCATT 420
Db 369 GGAGGAGCTTATCTTTATATATCTGCTTACCACACAGCAGAACTGGCAGGTGTCATT 428
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 480
Db 429 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 488
QY 481 AATAGAGATTTTCTATTTCTAGTCCAGCGGATTTGACCCCTTTGGTTCCCTCGATG 540
Db 489 AATAGAGATTTTCTATTTCTAGTCCAGCGGATTTGACCCCTTTGGTTCCCTCGATG 548
QY 541 TTTGGTCTCTACGGTGGAAACTAAACCAATTTGGTGAATCCAGCAATGACCTTT 600
Db 549 TTTGGTCTCTACGGTGGAAACTAAACCAATTTGGTGAATCCAGCAATGACCTTT 608
QY 601 AAAACCTATGAAGTATGATGACAGTTCTGCTCAACAGGAAATGATGATGTCAGCAA 660
Db 609 AAAACCTATGAAGTATGATGACAGTTCTGCTCAACAGGAAATGATGATGTCAGCAA 668
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RESULT 14

US-09-988-982-2
; Sequence 2, Application US/09988982
; Patent No. 6838245

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Shah, Purvi

Murry, Lynn E.

TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/988,982
APPLICATION NUMBER: 6838245-2001
FILING DATE: 19-NO. 6838245-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-988-982-2

Query Match 77.9%; Score 552.8; DB 3; Length 709;

Best Local Similarity 89.9%; Pred. No. 2.5e-180;

Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;

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QY 1 ATGTGGCGCAATAAATGATCAACCCCGCTGCCCGCATCGTGCCTCCGCGCCGCGGAGGCC 60
Db 75 ATGTGGCGCAATAAATGATCAACCCCGCTGCCCGCATCGTGCCTCCGCGCCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTTCTGCAATGATGGGAGATACCTGGGACCGATGGGAGGCC 120
Db 135 ACCGCTGCGGTGATTTTCTGCAATGATGGGAGATACCTGGGAGGCC 175
QY 121 TTTGCAGGTATCAGAAGTTACATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
Db 176 -----GCTGTAGGCT 188
QY 181 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCAACA 240
Db 189 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCAACA 248
QY 241 GATTACAGGAGGATGAATCTGGGATTAACACGCGACGAGAAATATAAAGCTTTGATT 300
Db 249 GATTACAGGAGGATGAATCTGGGATTAACACGCGACGAGAAATATAAAGCTTTGATT 308
QY 301 GATCAAGAGTGAAGATGCGATTCCTTCTAAGAAATATTTTGGAGGGTTTCTCAG 360
Db 309 GATCAAGAGTGAAGATGCGATTCCTTCTAAGAAATATTTTGGAGGGTTTCTCAG 368
QY 361 GGAGGAGCTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCATT 420
Db 369 GGAGGAGCTTATCTTTATATATCTGCTTACCACACAGCAGAACTGGCAGGTGTCATT 428
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 480
Db 429 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 488
QY 481 AATAGAGATTTTCTATTTCTAGTCCAGCGGATTTGACCCCTTTGGTTCCCTCGATG 540
Db 489 AATAGAGATTTTCTATTTCTAGTCCAGCGGATTTGACCCCTTTGGTTCCCTCGATG 548
QY 541 TTTGGTCTCTACGGTGGAAACTAAACCAATTTGGTGAATCCAGCAATGACCTTT 600
Db 549 TTTGGTCTCTACGGTGGAAACTAAACCAATTTGGTGAATCCAGCAATGACCTTT 608
QY 601 AAAACCTATGAAGTATGATGACAGTTCTGCTCAACAGGAAATGATGATGTCAGCAA 660
Db 609 AAAACCTATGAAGTATGATGACAGTTCTGCTCAACAGGAAATGATGATGTCAGCAA 668
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Job time : 219 secs

QY 661 TTCAATTGATAAACTCCTACTCTCAATTGATTGACGTCACTA 701
Db 669 TTCAATTGATAAACTCCTACTCTCAATTGATTGACGTCACTA 709

RESULT 15
US-09-949-016-122098
; Sequence 122098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122098
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122098

Query Match 70.4%; Score 500; DB 3; Length 601;
Best Local Similarity 97.5%; Pred. No. 4.2e-162;
Matches 517; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 182 TTACATTAATAATGAACGGTGTGCTATGCCCTTCATGGTTTGATATATTGGGCTTTCACCAG 241
Db 3 TAACATTAATAATGAACATAGCTATGCCCTTCATGGTTTGATATATTGGGCTTTCACCAG 62
QY 242 ATTCACAGGAGGATGAATCTGGGATTAACAGGCAGCAGAAATATAAAAGCTTTGATTG 301
Db 63 ATTCACAGGAGGATGAATCTGGGATTAACAGGCAGCAGAAATATAAAAGCTTTGATTG 122
QY 302 ATCAGAAGTGAAGATGGCATTCCTCTAACAGAAATATTTGGAGGGTTTCTCAGG 361
Db 123 ATCAGAAGTGAAGATGGCATTCCTCTAACAGAAATATTTGGAGGGTTTCTCAGG 182
QY 362 GAGGAGCTTTATCTTTATATATCTGCCCTTACCACACAGCAGAACTGGCAGGTGTCACTG 421
Db 183 GAGGAGCTTTATCTTTATATATCTGCCCTTACCACGACCAGAACTGGCAGGTGTCACTG 242
QY 422 CACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTCCACAGGGTCCATCGGTGGTGCTA 481
Db 243 CACTCAATTTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGGTCCATCGGTGGTGCTA 302
QY 482 ATAGAGATATTTCTATTTCTCCAGTCCAGGGATGTGACCCCTTTGGTTCCCTCGATGT 541
Db 303 ATAGAGATATTTCTATTTCTCCAGTCCAGGGATGTGACCCCTTTGGTTCCCTCGATGT 362
QY 542 TTGGTTCTCTTACGGTGGAAAACT-AAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 600
Db 363 TTGGTTCTCTTACGGTGGAAAACTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 422
QY 601 AAAACCTATGAAGGTATGATGACAGTTCTGTGTCAAAGAAATGATGGATGTCAAGCAA 660
Db 423 AAAACCTATGAAGGTATGATGACAGTTCTGTGTCAAAGAAATGATGGATGTCAAGCAA 482
QY 661 TTCAATTGATAAACTCCTACTCTCAATTGATTGACGTCACTAAGAGGCCCTT 710
Db 483 TTCAATTGATAAACTCCTACTCTCAATTGATTGACGTCACTAAGAGGCCCTT 532

Search completed: April 14, 2006, 13:40:30

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:20:28 ; Search time 3810 Seconds
(without alignments)
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Title: US-09-493-601B-1
Perfect score: 710
Sequence: 1 atgtgcggcaatacatgtc.....tgacgtcactaagagccctt 710

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708.4	99.8	760	8 AF291053	Homo sapi
2	708.4	99.8	1348	6 AX780008	Sequence
3	708.4	99.8	1381	8 BC010397	Homo sapi
4	708.4	99.8	1441	8 BC008652	Homo sapi
5	708.4	99.8	1486	6 AR079197	Sequence
6	708.4	99.8	1486	6 AR104347	Sequence
7	708.4	99.8	1486	6 BD191690	Human lys
8	708.4	99.8	1556	6 AR203099	Sequence
9	708.4	99.8	1556	8 AF052112	Homo sapi
10	708.4	99.8	2417	6 CQ894709	Sequence
11	708.4	99.8	2417	6 CQ896205	Sequence
12	708.4	99.8	2417	6 AR203084	Sequence
13	708.4	99.8	2417	6 AX256070	Sequence
14	708.4	99.8	2417	8 AF081281	Homo sapi
15	708.4	99.8	2600	6 CQ493329	Sequence
16	689.8	97.2	693	8 CR457103	Homo sapi
17	662.4	93.3	49616	8 AL365267	Human DNA
18	614	86.5	154252	8 AC004062	Homo sapi

19	602.8	84.9	2467	6 AX780162	AX780162 Sequence
20	596	83.9	660	4 OC97147	U97147 Oryctolagus
21	585.2	82.4	1940	9 BC085750	Rattus norv
22	585.2	82.4	2325	9 BC085750	D63885 Rat liver m
23	585.2	82.4	2356	9 RAT25KDL	BC013536 Mus muscu
24	580.4	81.7	2447	9 BC013536	BC052848 Mus muscu
25	578.8	81.5	2530	9 BC052848	BD134996 Human nuc
26	566.4	79.8	2408	6 BD134996	AX018183 Sequence
27	566.4	79.8	2408	6 AX018183	AR203091 Sequence
28	565	79.6	693	6 AR203091	U89352 Mus musculu
29	565	79.6	693	9 MMU89352	U97148 Oryctolagus
30	563.4	79.4	734	4 OC97148	CT010201 Mus muscu
31	561.4	79.1	693	9 CT010201	AR203102 Sequence
32	556.4	78.4	727	6 AR203102	AR028701 Sequence
33	552.8	77.9	709	6 AR028701	AR079196 Sequence
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35	552.8	77.9	709	6 AR104346	AR178569 Sequence
36	552.8	77.9	709	6 AR178569	BD191689 Human lys
37	552.8	77.9	709	6 BD191689	AR629275 Sequence.
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40	492.6	69.4	163364	14 AC116241	AC118319 Rattus no
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42	492.6	69.4	250178	14 AC118121	AC099137 Rattus no
43	481.6	67.8	233231	14 AC099137	AC073054 Homo sapi
44	432	60.8	154419	8 AC073054	AB168430 Macaca fa
45	423.8	59.7	2190	8 AB168430	

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LOCUS Homo sapiens acyl-protein thioesterase-1 mRNA, complete cds. PRI 20-NOV-2000
DEFINITION Homo sapiens acyl-protein thioesterase-1 mRNA, complete cds.
ACCESSION AF291053
VERSION AF291053.1 GI:9965371
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 760)
AUTHORS Devedjiev,Y., Dauter,Z., Kuznetsov,S.R., Jones,T.L. and Derwenda,Z.S.
TITLE Crystal structure of the human acyl protein thioesterase I from a single X-ray data set to 1.5 A
JOURNAL Structure Fold. Des. 8 (11), 1137-1146 (2000)
PUBMED 11080636
REFERENCE 2 (bases 1 to 760)
AUTHORS Kuznetsov,S.R. and Jones,T.L.Z.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2000) Metabolic Disease Branch, National Institute of Diabetes and Digestive and Kidney Diseases, 9000 Rockville Pike, Bldg.10, Room 9C112, Bethesda, MD 20892, USA

FEATURES

source

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Best Local Similarity 99.9%; Pred. No. 1.4e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 19 ATGTGCGGCAATAACATGTCACCCGCTGCCCGCATCGTGCCGCCGCCGCGGAGGCC 78
QY 61 ACCGCTGCGGTGATTTCTGTCATGATGGAGATCTGGGACGATGGGACGAGGCC 120
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LOCUS
Sequence 2165 from Patent WO03039443.
AX780008
AX780008.1 GI:32697002
KEYWORDS
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1
Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,
Dugas, M., Bils, R., Brors, B. and Mergenthaler, S.

Novel genetic markers for leukemias
Patent: WO 03039443-A 2165 15-MAY-2003;
Deutsches Krebsforschungszentrum (DKFZ);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten,
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
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location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 6 ATGTGCGGCAATAACATGTCACCCGCTGCCCGCATCGTGCCGCCGCCGCGGAGGCC 65
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QY 181 GTTACATTAATATGAACGTGGCTATGCTTCATGCTTGTATATTTGGGCTTTCACCA 240
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DB 366 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGCGAGGTGCACCT 425
QY 421 GCACCTAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCCTATCGGTGGTCT 480
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QY 481 AATAGAGATTTCTATTCTTCCAGTCCCAACGGGGATTGTGACCCCTTTGGTTCCCTGTATG 540
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QY 661 TTCAATTGATAAACTCCTACCTCAATTTGATTGACGTCACCTAAGAGGCCCTT 710
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BC010397
LOCUS
DEFINITION
Homo sapiens lysophospholipase I, mRNA (cDNA clone MGC:13688
IMAGE:4109335), complete cds.
ACCESSION
BC010397
VERSION
BC010397.1 GI:14714525
KEYWORDS
MGC.

SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo
1 (bases 1 to 1381)

REFERENCE
AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Holtzman, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Spletten, M., Soares, M.B., Donald, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Udell, J., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S., Bosak, S.A., McSwan, P.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vitaloni, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Mammalian
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED

12477932

2 (bases 1 to 1381)

Strausberg, R.

Direct Submission

Submitted (09-JUL-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

<http://www.systemsbio.org>

Contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 19 Row: f Column: 5

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 20302148.

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REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 1441) Strausberg R.L., Fellings, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wegner, L., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wille, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kerteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smail, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLID	12477932
REFERENCE	2 (bases 1 to 1441)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC project URL: http://mgc.nci.nih.gov
COMMENT	On Aug 25, 2003 this sequence version replaced gi:14250433. Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: e Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20302148. Location/Qualifiers 1. .1441 /organism="Homo sapiens" /mol_type="mRNA" /clone="MGC:9121 IMAGE:3865775" /issue_type="Eye, retinoblastoma" /clone_lib="NIH MGC_67" /lab_host="DH10B" /note="Vector: pCMV-SPORT6" 1. .1441 /genes="LYPLA1" /note="synonyms: LPL1, APT-1, LYSOPLA" /db_xref="GeneID:10434" /db_xref="MIM:605599" 83..775 /genes="LYPLA1" /codon_start=1 /product="lysophospholipase I" /protein_id="AAH08652.1"
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CDS	

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ORIGIN	
Query Match	99.8%; Score 708.4; DB 8; Length 1441;
Best Local Similarity	99.9%; Pred. No. 1.5e-190;
Matches	709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 ATGTGGCGCAATAAATGTCACCGCGCTGCGCGCATCGTCCCGCGCCCGCGAAGGCC 60
Db	83 ATGTGGCGCAATAAATGTCACCGCGCTGCGCGCATCGTCCCGCGCCCGCGAAGGCC 142
QY	61 ACCGCTGGCGGTGATTTCTCTGTCATGATTTGGGAGATATCTGGGCACCGGATGGCAGAAGCC 120
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QY	121 TTTGAGGTATCAGAAAGTTTCACATATCAATATATCTGCCGCATGCGCCTGTAGGCTT 180
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QY	181 GTTACATTAAATATGAAGTGGCTATGCTTCATGTTTATGATTATTTGGGCTTTTCCACCA 240
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QY	241 GATTCACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAAATATAAAGCTTTTGATT 300
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QY	301 GATCAAGAGTGAAGATGGCATTCCTTCTTAACAGAAATATTTTGGGAGGTTTCTCAG 360
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QY	361 GGAGAGCTTTTATCTTTTATATATCTCCCTTACCACACAGCAAAATGCGAGGTGCCT 420
Db	443 GGAGAGCTTTTATCTTTTATATCTCCCTTACCACACAGCAAAATGCGAGGTGCCT 502
QY	421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGT 480
Db	503 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGT 562
QY	481 AATAGAGATATTTCTTATCTCCAGTGCACGGGGATTTGTGACCCCTTTGGTTCCCTCGATG 540
Db	563 AATAGAGATATTTCTTATCTCCAGTGCACGGGGATTTGTGACCCCTTTGGTTCCCTCGATG 622
QY	541 TTTGGTCTCTTACCGTGGAAAACTAAAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
Db	623 TTTGGTCTCTTACCGTGGAAAACTAAAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 682
QY	601 AAAACCTATGAAGGTATGATGACAGTTCTGCTCAACAGGAAATGATGATGTCTCAAGCAA 660
Db	683 AAAACCTATGAAGGTATGATGACAGTTCTGCTCAACAGGAAATGATGATGTCTCAAGCAA 742
QY	661 TTCATTGATAAACTCCTACCTCCAATGATTGACGTCACTAAGAGGCCCTT 710
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LOCUS	AR079197 1486 bp DNA linear PAT 31-AUG-2000
DEFINITION	Sequence 4 from patent US 5965423.
ACCESSION	AR079197
VERSION	AR079197.1 GI:10005943
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.

REFERENCE 1 (bases 1 to 1486)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 5965423-A 4 12-OCT-1999;
FEATURES Location/Qualifiers
source 1..1486
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 99.8%; Score 708.4; DB 6; Length 1486;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCACATGTCACCCCGCTGCCCGCATCGTGCCTCCCGCCCGCGAAGGCC 60
DB 76 ATGTGCGGCATTAATGTCACATGTCACCCCGCTGCCCGCATCGTGCCTCCCGCCCGCGAAGGCC 135
QY 61 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 120
DB 136 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 195
QY 121 TTTCAGAGTATCAGAGTTTACATATCAATATATCTGCCCGCATCGCTGTTAGGCCT 180
DB 196 TTTCAGAGTATCAGAGTTTACATATCAATATATCTGCCCGCATCGCTGTTAGGCCT 255
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DB 376 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATATTTTGGAGGGTTTCTCAG 435
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAGAGAACTGGCAGGTGCAC 420
DB 436 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAGAGAACTGGCAGGTGCAC 495
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGGTCTTATCGGTGGTCT 480
DB 496 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGGTCTTATCGGTGGTCT 555
QY 481 AATAGAGATTTCTATTTCTCCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATG 540
DB 556 AATAGAGATTTCTATTTCTCCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATG 615
QY 541 TTTGGTCTCTTACGGTGGAAACTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 600
DB 616 TTTGGTCTCTTACGGTGGAAACTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 675
QY 601 AAAACCTATGAAGTATGATGACAGTTTCGTGTCACAGGAAATGATGATGTCAGCA 660
DB 676 AAAACCTATGAAGTATGATGACAGTTTCGTGTCACAGGAAATGATGATGTCAGCA 735
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DB 736 TTCATTGATAAATCTCTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 785

RESULT 6
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LOCUS AR104347 1486 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6093561.
ACCESSION AR104347
VERSION AR104347.1 GI:12817055
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1486)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 6093561-A 4 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..1486
/organism="unknown"
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ORIGIN

Query Match 99.8%; Score 708.4; DB 6; Length 1486;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCACATGTCACCCCGCTGCCCGCATCGTGCCTCCCGCCCGCGAAGGCC 60
DB 76 ATGTGCGGCATTAATGTCACATGTCACCCCGCTGCCCGCATCGTGCCTCCCGCCCGCGAAGGCC 135
QY 61 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 120
DB 136 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 195
QY 121 TTTCAGAGTATCAGAGTTTACATATCAATATATCTGCCCGCATCGCTGTTAGGCCT 180
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DB 316 GATTTCACAGAGGATGAATCTGGGATTTAAACAGGACGAGAGAAATATAAAGCTTTTGATT 375
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DB 436 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAGAGAACTGGCAGGTGCAC 495
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RESULT 7
BD191690
LOCUS BD191690 1486 bp DNA linear PAT 17-JUL-2003
DEFINITION Human lysophospholipase.
ACCESSION BD191690
VERSION BD191690.1 GI:33001429
KEYWORDS JP 2002514081-A/2.
SOURCE unidentified
ORGANISM unclassified.


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Db 396 GGAGGAGCTTTATCTTTATATCTGCTTATCTGCTTACACACAGCAGAAACTGGCAGGTGTCACT 455
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LOCUS CQ896205
DEFINITION Sequence 29 from Patent WO2004076614.
ACCESSION CQ896205
VERSION CQ896205.1 GI:55468054
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hinzmann,B., Dahl,E., Rosenthal,A., Specht,T., Schmitt,A., Beckmann,G., Bruemendorf,T., Kinnemann,H., Roepcke,S., Hermann,K., Xinzhong,L., Pillarsky,C. and Staub,E.
TITLE Human nucleic acid sequences obtained from prostatic carcinomas
JOURNAL Patent: WO 2004076614-A 29 10-SEP-2004; Rosenthal, Andre (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE); Specht, Thomas (DE); Schmitt, Armin (DE)
FEATURES
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ORIGIN
Query Match 99.8%; Score 708.4; DB 6; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.6e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAACAATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCGCCGCGGGAAGGCC 60
Db 36 ATGTGCGGCAATAAACAATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCGCCGCGGGAAGGCC 95
QY 61 ACCGCTCGCGTGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
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RESULT 12
LOCUS AR203084
DEFINITION Sequence 3 from patent US 6365354.
ACCESSION AR203084
VERSION AR203084.1 GI:21499381
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2417)
AUTHORS Bennett,C.Frank. and Wyatt,J.
TITLE Antisense modulation of lysophospholipase I expression
JOURNAL Patent: US 6365354-A 3 02-APR-2002;
FEATURES
source 1..2417
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ORIGIN
Query Match 99.8%; Score 708.4; DB 6; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.6e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAACAATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCGCCGCGGGAAGGCC 60
Db 36 ATGTGCGGCAATAAACAATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCGCCGCGGGAAGGCC 95
QY 61 ACCGCTCGCGTGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
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Db 156 TTTGCAAGGTATCAGAGTTTCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAAT 215
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QY      481 AATAGAGATATTTCTATTTCTCAGTCCACGGGATTTGACCCCTTTGGTTCCTCCGTGATG 540
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RESULT 13
AX256070 LOCUS 2417 bp DNA linear PAT 10-OCT-2001
Sequence 221 from Patent WO0170976.
AX256070 DEFINITION
AX256070 HOMO sapiens (human)
AX256070.1 GI:16075110
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Xu,J., Pyle,R.A. and Stolk,J.A.
AUTHORS Compositions and methods for the therapy and diagnosis of ovarian
TITLE and endometrial cancer
JOURNAL Patent: WO 0170976-A 221 27-SEP-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..2417
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ORIGIN
Query Match 99.8%; Score 708.4; DB 6; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.6e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGGGCAATACATGTCAACCCCGCTGCCCGCATCGTCCCGCCCGGAGGCC 60
Db 36 ATGTGGGCAATACATGTCAACCCCGCTGCCCGCATCGTCCCGCCCGGAGGCC 95
QY 61 ACCGCTCGGTGATTTTCTGATGATTCGGAGATCTGGCAGCATGGCAGAGGCC 120
Db 96 ACCGCTCGGTGATTTTCTGATGATTCGGAGATCTGGCAGCATGGCAGAGGCC 155
QY 121 TTTGCAAGTATCAGAAAGTTCAATATATATCTGCGCGCATGCGCCTGTAGGCTT 180
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DEFINITION Homo sapiens lysophospholipase (LPL1) mRNA, complete cds.
ACCESSION AF081281
VERSION AF081281.1 GI:3415122
KEYWORDS SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2417)
REFERENCE Hu,G.
AUTHORS Direct Submission
TITLE Submitted (02-AUG-1998) Shanghai Institute of Cell Biology, 320
JOURNAL Yue-Yang Road, Shanghai 200031, China
FEATURES Location/Qualifiers
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RESULT 15
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LOCUS
Sequence 25196 from Patent WO0160860.
DEFINITION
CQ493329
ACCESSION
CQ493329.1 GI:41458948
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1
Schlegel, R., Endege, W.O. and Monahan, J.E.
AUTHORS
Genes differentially expressed in human prostate cancer and their
TITLE
use

JOURNAL Patent: WO 0160860-A 25196 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES
Source
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ORIGIN

Query Match	99.8%;	Score	708.4;	DB	6;	Length	2600;		
Best Local Similarity	99.9%;	Pred. No.	1.6e-190;						
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Qy	1	ATGTGCGGCAATAACATGTCAACCCCGCTGCCCGCCATCGTGGCCGCGCCGGAAGGCC	60						
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Qy	61	ACCGCTGCGGTGATTTTCTGTCATGGATTTGGGAGATACTGGGCACGGATGGGCGAAGGCC	120						
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Qy	121	TTTTCAGGATACAGAAAGTTACATATCAAAATATATCTGCCCGCATCGCCTGTTAGGCCT	180						
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Qy	181	GTTCACATTAATATGAACGTGGCTATGCCCTTCATGGTTTCATATTTGGGCTTTTCACCA	240						
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Qy	241	GATTCACAGGAGATGAATCTGGGATTAACAGGCGACAGAAAATATAAAGCTTTTGATT	300						
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Qy	301	GATCAAGAGTGAAGAAATGGCAATTCCTTCTAAACAGAAATTAATTTGGGAGGGTTTCTCAG	360						
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Qy	361	GGAGGAGCTTTATCTTTTATATCTGCCCTTACCACAGCAGAGAACTGGCAGGTGTCACT	420						
Db	523	GGAGGAGCTTTATCTTTTATATCTGCCCTTACCACAGCAGAGAACTGGCAGGTGTCACT	582						
Qy	421	GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGGTGCT	480						
Db	583	GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGGTGCT	642						
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Job time : 3815 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:17:45 ; Search time 587 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
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12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	710	100.0	758	AAH26336	Aah26336 Human bra
2	708.4	99.8	1348	ADP81609	Adf81609 Leukaemia
3	708.4	99.8	1486	AAH56267	Aax56267 Human lys
4	708.4	99.8	1486	ACC82267	Acc82267 Human NOV
5	708.4	99.8	1486	ADT71491	Adt71491 Human lys
6	708.4	99.8	1556	ABK37045	Abk37045 DNA encod
7	708.4	99.8	2415	ADO87736	Adg87736 Human tum
8	708.4	99.8	2417	AAH56597	Aas56597 Human cdn
9	708.4	99.8	2417	ABK37030	Abk37030 DNA encod
10	708.4	99.8	2417	ABL59514	AbL59514 Human lys
11	708.4	99.8	2417	ADR65833	Adr65833 Human pro
12	708.4	99.8	2417	ADR66517	Adr66517 Human pro
13	708.4	99.8	2417	ADX97471	Adx97471 Pancreat
14	708.4	99.8	2493	ACAC98208	Aac98208 Human col
15	708.4	99.8	2578	ACN38804	Acn38804 Tumour-as
16	708.4	99.8	2600	ABV5207	Abv5207 Human pro
17	686.4	96.7	1538	AAS71464	Aas71464 DNA encod
18	668.4	94.1	701	ACC62265	Acc62265 Human NOV
19	668.4	94.1	701	ADH47693	Ade47693 Human NOV

20	668.4	94.1	701	12	ADJ78963	Adj78963 Human NOV
21	604.4	85.1	2417	8	ACC49478	Acc49478 Human lys
22	602.8	84.9	2467	10	ADF81763	Adf81763 Leukaemia
23	602.4	84.8	1300	3	AAZ61501	Aaz61501 cDNA enco
24	565	79.6	693	6	ABK37037	Abk37037 DNA encod
25	565	79.6	2396	4	AAH34424	Aah34424 Human col
26	556.4	78.4	727	6	ABK37048	Abk37048 DNA encod
27	552.8	77.9	709	2	AAH56266	Aax56266 Human lys
28	495.2	69.7	521	14	ADV74708	Adv74708 Human col
29	408.8	57.6	616	8	ACC62266	Acc62266 Human NOV
30	404.6	57.0	419	6	ABL37780	AbL37780 Human col
31	397.4	56.0	470	14	ADV74570	Adv74570 Human col
32	343.4	48.4	441	8	ABX38759	Abx38759 Bovine ES
33	337.2	47.5	662	13	ADO54630	Add54630 Novel can
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36	277.6	39.1	1622	12	ADQ87643	Adq87643 Human tum
37	277.6	39.1	1624	4	AAC60229	Aac60229 Human hyd
38	277.6	39.1	1824	10	ADB90836	AdB90836 Human CDN
39	277.6	39.1	1625	10	ADH61157	Adh61157 Human hyd
40	277.6	39.1	1647	6	ABL59535	AbL59535 Human lys
41	277.6	39.1	1648	13	ACN37299	Acn37299 Tumour-as
42	263.2	37.1	1624	12	ADQ83757	Adq83757 Human tum
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44	200.2	28.2	1061	13	ADQ83758	Adq83758 Human tum
45	200.2	28.2	1061	13	ACN38433	Acn38433 Tumour-as

ALIGNMENTS

RESULT 1
AAH26336
ID AAH26336 standard; cDNA; 758 BP.
XX
AC AAH26336;
XX
DT -02-OCT-2001 (first entry)
XX
DE Human brain lysophospholipase cDNA.
XX
KW Lysophospholipase; human; brain; lysophospholipid; atherosclerosis;
KW hyperlipidaemia; dysrhythmia; myocardial ischaemia; demyelination;
KW vasotropic; antiatherosclerotic; antilipaemic; neuroprotective;
KW gene therapy; LysoPLA; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
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FT 741 is specifically claimed in Claim 1"
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FT primer_bind /*tag= c
WO2001515166-A1.
02-AUG-2001.
28-JAN-2000; 2000WO-US002319.
28-JAN-2000; 2000US-00493601.
(REGC) UNIV CALIFORNIA.
Dennis EA, Wang A;
WPI; 2001-483215/52.
P-PSDB; AAB82669.
XX


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Db      616  TTTGGTTCTCTACGGTGAAAAAATCTAAAAAATTTGGTGAATCCAGCCCAATGTGACCTTT 675
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Db      676  AAAACCTATGAAGGTATGATGCACAGTTCGTGTCACAGGAATGATGATGTCACAGCAA 735
QY      661  TTCATTGATAAACTCTACTCTCAATGATTGACGTCACCTAAGAGGCTTT 710
Db      736  TTCATTGATAAACTCTACTCTCAATGATTGACGTCACCTAAGAGGCTTT 785

RESULT 4
ACC62267
ID      ACC62267 standard; cDNA; 1486 BP.
XX
AC      ACC62267;
XX
DT      23-JUN-2003 (first entry)
XX
DE      Human NOV7c encoding cDNA SEQ ID NO:63.
XX
KW      Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW      anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW      haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW      neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaeamic;
KW      gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW      congenital heart defect; aortic stenosis; valve disease; transplantation;
KW      tuberosus sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW      prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW      fertility; haemophilia; hypercoagulation; graft versus host disease;
KW      idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW      Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW      cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW      immune disorder; haematopoietic disorder; dyslipidaemia;
KW      metabolic syndrome X; gene; ss.
XX
XX      Homo sapiens.
XX
XX      WO2003023001-A2.
XX
XX      20-MAR-2003.
XX
PF      09-SEP-2002; 2002WO-US028538.
XX
XX      07-SEP-2001; 2001US-0318120P.
PR      07-SEP-2001; 2001US-0318184P.
PR      10-SEP-2001; 2001US-0318430P.
PR      17-SEP-2001; 2001US-0322636P.
PR      17-SEP-2001; 2001US-0322781P.
PR      17-SEP-2001; 2001US-0322816P.
PR      17-SEP-2001; 2001US-0322817P.
PR      19-SEP-2001; 2001US-0323519P.
PR      20-SEP-2001; 2001US-0323631P.
PR      20-SEP-2001; 2001US-0323636P.
PR      25-SEP-2001; 2001US-0324969P.
PR      25-SEP-2001; 2001US-0325091P.
PR      26-SEP-2001; 2001US-0324990P.
PR      14-DEC-2001; 2001US-0341144P.
PR      26-FEB-2002; 2002US-0359599P.
PR      05-MAR-2002; 2002US-0361863P.
PR      03-MAY-2002; 2002US-0377901P.
PR      17-MAY-2002; 2002US-0381483P.
PR      29-MAY-2002; 2002US-0383863P.
PR      02-JUL-2002; 2002US-0393332P.
PR      17-JUL-2002; 2002US-0396412P.

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PR      13-AUG-2002; 2002US-0403517P.
XX      06-SEP-2002; 2002US-00236417.
XX
XX      (CURA-) CURAGEN CORP.
XX
PI      Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI      Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI      Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI      Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI      Kekuda R, Khramtsov NV, Leach MD, Lopley DM, Li L, Liu X;
PI      Malyankar UM, Miller CE, Ooi CE, Ort T, Padigar M, Patturajan M;
PI      Pena CE, Rieger DK, Rothenberg MB, Shenoy SC, Shmkeles RA;
PI      Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI      Zerhusen BD, Zhong M;
XX
XX      WPI; 2003-313241/30.
DR      P-PSDB; ABR54198.
XX
XX      Novel human proteins and nucleic acid encoding the proteins, useful for
XX      diagnosis, treatment and prevention of disorders involving the human
XX      protein or nucleic acid e.g. cardiac and neurological disorders.
XX
XX      Claim 20; Page 129-130; 460pp; English.
XX
XX      The present invention describes isolated human NOVX proteins, where X is
XX      1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
XX      ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
XX      hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
XX      antidiabetic, antiinfertility, haemostatic, neuroprotective, anti-HIV,
XX      antiasthmatic, metabolic, immunomodulator, antiparkinsonian, nootropic,
XX      antiparkinsonian and antilipaeamic activities, and can be used in gene
XX      therapy. NOVX proteins are useful for treating or preventing a pathology
XX      associated with a NOVX protein in humans and for treating a syndrome
XX      associated with the human disease. NOVX nucleic acids, proteins and
XX      antibodies can be used in the treatment and diagnosis of cardiomyopathy,
XX      atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
XX      valve disease, tuberosus sclerosis, scleroderma, obesity, transplantation,
XX      congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
XX      disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
XX      hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
XX      disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
XX      infectious disease, anorexia, cancer-associated cachexia, cancer,
XX      Alzheimer's disease, Parkinson's disease, immune disorders,
XX      haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
XX      ACC62345 to ACC62465 represent PCR primers and probes for human NOVX
XX      sequences, which are used in examples from the present invention.
XX      ABR54277 represents a human crypsinogen protein given in comparison with
XX      the human NOV35b protein in the exemplification of the present invention
XX
XX      Query Match          99.8%; Score 708.4; DB 8; Length 1486;
XX      Best Local Similarity 99.9%; Pred. No. 1.3e-221;
XX      Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1      ATGTGCGGCAATAAATGTCACCCCGCTGCCCGCATCGTGC CGCCCGCGGAAGGCC 60
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Db      136      ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTG GGGCAGCGATGGGAGAGCC 195
QY      121      TTTCAGGATATCAGAGTTTCACATATCAATATCTGCGCGCATCGTGC CGCTGTTAGSCCT 180
Db      196      TTTCAGGATATCAGAGTTTCACATATCAATATCTGCGCGCATCGTGC CGCTGTTAGSCCT 255
QY      181      GTTACATTAAATATGAACGTGGCTATGCGCTTTCATGTTTCATATTTGATTTTGGCTTTTCCACCA 240
Db      256      GTTACATTAAATATGAACGTGGCTATGCGCTTTCATGTTTCATGTTTGTATTTTGGCTTTTCCACCA 315
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Db 436 GGAGGAGCTTTATCTTTTATATCTGCCCCCTTACACACAGAGAACTGGCAGGTGTCACT 495
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QY 481 AATAGAGATATTCTTATCTTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 540
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QY 661 TTCAATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACTTAAGAGGCCCTT 710
Db 736 TTCAATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACTTAAGAGGCCCTT 785

RESULT 5

ADT71491
ID ADT71491 standard; DNA; 1486 BP.
XX AC ADT71491;
XX AC ADT71491;
DT 30-DEC-2004 (first entry)
XX DE Human lysophospholipase 1 gene SEQ ID NO:10.

XX ds; gene; LYPLAL1; lysophospholipase 1; psychoactive; antidepressant;
KW neuroleptic; analgesic; opioid modulator; psychoactive;
KW psychiatric disorder; depression; schizophrenia; pain.
XX Homo sapiens.

XX WO2004088274-A2.
XX 14-OCT-2004.
XX 26-MAR-2004; 2004WO-US009042.
XX 26-MAR-2003; 2003US-0457753P.
XX (CURA-) CURAGEN CORP.
XX Gunther E, Stone DJ, Gerwien RW;
XX WPI; 2004-748157/73.

XX Identifying a psychoactive compound, useful for treating psychiatric
PT disorders e.g., depression, comprises contacting a cell with a test
PT compound and determining expression level of a psychoactive-associated
PT gene in the cell.

XX Claim 8; SEQ ID NO 10; 31pp; English.
XX The invention relates to a novel method for identifying a psychoactive
CC compound comprising contacting a cell with a test compound and
CC determining a level of expression of a psychoactive-associated gene in
CC the cell, where an increase or decrease of the level compared to a normal
CC control level of the gene indicates that the test compound is a

CC psychoactive compound. A compound of the invention has antidepressant,
CC neuroleptic, and analgesic activity, and acts as a opioid modulator, and
CC psychoactive. The method is useful for identifying a psychoactive
CC compound or identifying drug efficacy of a psychoactive compound for
CC treating psychiatric disorders of depression, schizophrenia and pain. The
CC present sequence represents a human psychoactive-associated gene,
CC lysophospholipase 1 (LYPLAL1).

XX SQ Sequence 1486 BP; 418 A; 304 C; 300 G; 459 T; 0 U; 5 Other;

Query Match 99.8%; Score 708.4; DB 13; Length 1486;
Best Local Similarity 99.9%; Pred. No. 1.3e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCACACCGCTGCCCGCATCGTGCCTCCCGCCGGAAGGCC 60
Db 76 ATGTGCGGCAATAAATGTCACACCGCTGCCCGCATCGTGCCTCCCGCCGGAAGGCC 135
QY 61 ACCGCTGCGGTGATTTCTCTGATGAGTTGGGAGATCTGGGACAGGATGGGAGGCC 120
Db 136 ACCGCTGCGGTGATTTCTCTGATGAGTTGGGAGATCTGGGACAGGATGGGAGGCC 195
QY 121 TTTGCGAGGTATCAGAAATTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCCT 180
Db 196 TTTGCGAGGTATCAGAAATTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCCT 255
QY 181 GTTACATTAATTAATGAACGTGCTATGCCTTCATGGTTGATATATTGGGCTTTTCAACA 240
Db 256 GTTACATTAATTAATGAACGTGCTATGCCTTCATGGTTGATATATTGGGCTTTTCAACA 315
QY 241 GATTACAGGAGATGAATCTGGGATTAACAGGCGAGCAAGAAATATAAAGCTTTGATT 300
Db 316 GATTACAGGAGATGAATCTGGGATTAACAGGCGAGCAAGAAATATAAAGCTTTGATT 375
QY 301 GATCAAGAGTGAAGATGGCAATTCCTTCTAACAGAAATTAATTTGGGAGGGTTTCTCAG 360
Db 376 GATCAAGAGTGAAGATGGCAATTCCTTCTAACAGAAATTAATTTGGGAGGGTTTCTCAG 435
QY 361 GGAGGAGCTTTATCTTTTATATCTGCCCCCTTACACACAGAGAACTGGCAGGTGTCACT 420
Db 436 GGAGGAGCTTTATCTTTTATATCTGCCCCCTTACACACAGAGAACTGGCAGGTGTCACT 495
QY 421 GCACCTAGTGTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGCTGCT 480
Db 496 GCACCTAGTGTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGCTGCT 555
QY 481 AATAGAGATATTCTTATCTTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 540
Db 556 AATAGAGATATTCTTATCTTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 615
QY 541 TTTGGTTCTTTACGGTGAAGAACTAAAAACAATTGGTGAATCCAGGCAATGTGACCTTT 600
Db 616 TTTGGTTCTTTACGGTGAAGAACTAAAAACAATTGGTGAATCCAGGCAATGTGACCTTT 675
QY 601 AAAACCTATGAGGTATGATGACACAGTTCGTGTCAACAGGAAATGATGTCAAGCAA 660
Db 676 AAAACCTATGAGGTATGATGACACAGTTCGTGTCAACAGGAAATGATGTCAAGCAA 735
QY 661 TTCAATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACTTAAGAGGCCCTT 710
Db 736 TTCAATTGATAAACTCCTACTCCTCAATTTGATTGACGTCACTTAAGAGGCCCTT 785

RESULT 6

ABK37045
ID ABK37045 standard; cDNA; 1556 BP.

XX AC ABK37045;

XX AC ABK37045;

XX 08-MAY-2002 (first entry)

XX DNA encoding human lysophospholipase I #3.

XX XX

KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic; 614
KW antilipaemic; cardiant; lysophospholipase I; inflammation; ischaemia;
KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
KW antisense gene therapy; gene; ss.
OS Homo sapiens.
PN WO200210185-A1.
XX 07-FEB-2002.
XX 20-JUL-2001; 2001WO-US022975.
XX 31-JUL-2000; 2000US-00629645.
XX (ISIS-) ISIS PHARM INC.
PA Bennett CF, Wyatt JR;
XX PI
XX DR WPI: 2002-188720/24.
XX DR P-PSDB; AAU85134.
XX
PT Novel antisense compound useful for treating inflammation,
PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
PT myocardial ischemia, inhibits Lysophospholipase I.
XX Example 15; Page 95-96; 131pp; English.
XX
CC The invention relates to an antisense compound (I) 8-30 nucleobases in
CC length targeted to a nucleic acid molecule encoding lysophospholipase I
CC (II), where (I) specifically hybridises with and inhibits the expression
CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
CC tissues, and for treating a human having a disease or condition
CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
CC and cardiovascular disorders such as atherosclerosis and myocardial
CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
CC useful for distinguishing functions of various members of a biological
CC pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
CC represent lysophospholipase I coding sequences, antisense
CC oligonucleotides and related PCR primers of the invention
XX
SQ Sequence 1556 BP; 423 A; 324 C; 350 G; 459 T; 0 U; 0 Other;
Query Match 99.8%; Score 708.4; DB 6; Length 1556;
Best Local Similarity 99.9%; Pred. No. 1.3e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCCGCGGAAGGCC 60
DB 195 ATGTGCGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCCGCGGAAGGCC 254
QY 61 ACCGTGCGGTGATTTTCTCGATGATGATGGAGATACCTGGGCACGGATGGGCAGAGCC 120
DB 255 ACCGTGCGGTGATTTTCTCGATGATGATGGAGATACCTGGGCACGGATGGGCAGAGCC 314
QY 121 TTTGAGGTATCAGAGTTTCAAT 180
DB 315 TTTGAGGTATCAGAGTTTCAAT 374
QY 181 GTTACATTAATAATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 375 GTTACATTAATAATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
QY 241 GATTACAGAGATGAATCTGGGATTAACAGGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 435 GATTACAGAGATGAATCTGGGATTAACAGGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 494
QY 301 GATCAGAGATGAGAGTGGATTCCTTCTACAGAAATATTTTGGAGGTTTCTCAG 360
DB 495 GATCAGAGATGAGAGTGGATTCCTTCTACAGAAATATTTTGGAGGTTTCTCAG 554
QY 361 GGAGAGGCTTATCTTTAT 420

DB 555 GGAGGAGCTTTATCTTTAT 614
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTCTATCGGTGGTCT 480
DB 615 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTCTATCGGTGGTCT 674
QY 481 AATAGAGATATTTCTATTTCTCCAGTGCACCGGGATTTGACCCCTTTGGTTCCCTCGATG 540
DB 675 AATAGAGATATTTCTATTTCTCCAGTGCACCGGGATTTGACCCCTTTGGTTCCCTCGATG 734
QY 541 TTTGGTCTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 600
DB 735 TTTGGTCTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 794
QY 601 AAAACCTATGAGGTATGATGCACAGTTTCGTGTCAACAGGAAATGATGATGATGATGATG 660
DB 795 AAAACCTATGAGGTATGATGCACAGTTTCGTGTCAACAGGAAATGATGATGATGATGATG 854
QY 661 TTCATTGATAAACTCCTACCTCCAATTGATTGACCTCACTAAGAGGCCCTT 710
DB 855 TTCATTGATAAACTCCTACCTCCAATTGATTGACCTCACTAAGAGGCCCTT 904
RESULT 7
ADQ87736
ID ADQ87736 standard; cDNA; 2415 BP.
XX AC ADQ87736;
XX
XX 07-OCT-2004 (first entry)
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4614.
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
PN WO2004060270-A2.
XX 22-JUL-2004.
XX 15-OCT-2003; 2003WO-US029126.
XX 18-OCT-2002; 2002US-0418988P.
XX (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX Wu TD, Zhou Y;
XX WPI: 2004-534300/51.
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX Claim 1; SEQ ID NO 4614; 5504pp; English.
XX The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a) -
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAR)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAR binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein.
CC Described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAR sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAR cDNA sequence from the present invention.
XX
SQ

Sequence 2415 BP; 750 A; 414 C; 421 G; 830 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 12; Length 2415;
Best Local Similarity 99.9%; Pred. No. 1.7e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAACATGTCAACCCCGCTGCCGCCATCGTCCCGCCCGGGAAGGCC 60
DB 36 ATGTGCGGCAATAACATGTCAACCCCGCTGCCGCCATCGTCCCGCCCGGGAAGGCC 95
QY 61 ACCGCTGCGGTGATTTTCTGCGATGATTTGGGAGATCTGGGCACCGATGGGCAAGCC 120
DB 96 ACCGCTGCGGTGATTTTCTGCGATGATTTGGGAGATCTGGGCACCGATGGGCAAGCC 155
QY 121 TTTCAGGATACAGAGTTTACATATCAATATATCTGCCGATCGCTGTGGCTT 180
DB 156 TTTCAGGATACAGAGTTTACATATCAATATATCTGCCGATCGCTGTGGCTT 215
QY 181 GTTACATTAATAATGAACGTGGCTATGCTTCTATGTTTGTATTTGGGCTTTTCCACCA 240
DB 216 GTTACATTAATAATGAACGTGGCTATGCTTCTATGTTTGTATTTGGGCTTTTCCACCA 275
QY 241 GATTTCACAGAGGATGAATCTGGGATTAACAGGCGAGCAAAAATATAAAGCTTTGATT 300
DB 276 GATTTCACAGAGGATGAATCTGGGATTAACAGGCGAGCAAAAATATAAAGCTTTGATT 335
QY 301 GATCAGAGAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 336 GATCAGAGAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGAGGGTTTCTCAG 395
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTACACAGAGCAAACTGGCAGGTGTCACT 420
DB 396 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGAGCAAACTGGCAGGTGTCACT 455
QY 421 GCATCAGTGTGCTTCACTTCGCGGTTCCTTCCACAGGGTCTTATCGGTGTGCT 480
DB 456 GCATCAGTGTGCTTCACTTCGCGGTTCCTTCCACAGGGTCTTATCGGTGTGCT 515
QY 481 AATAGAGATTTTCTATCTCCAGTCCCGGGATGTGACCTTTGGTTCCTCCCTGATG 540
DB 516 AATAGAGATTTTCTATCTCCAGTCCCGGGATGTGACCTTTGGTTCCTCCCTGATG 575
QY 541 TTTGGTCTCTTACGGTGGAAAAAATAAATCTTGTGAATCCAGCAATGTGACCTTT 600
DB 576 TTTGGTCTCTTACGGTGGAAAAAATAAATCTTGTGAATCCAGCAATGTGACCTTT 635
QY 601 AAAACCTATGAAGGTATGATGCAAGTTCTGTCAACAGGAAATGATGGATGCAAGCAA 660

DB 636 AAAACCTATGAAGGTATGATGACAGTTCTGTCTAACAGGAATGATGATGTCACAGCAA 695
QY 661 TTTCATTGATAAACTCTACCTCCAAATTTGATTGATGACGTCACTAAGAGGCTTT 710
DB 696 TTTCATTGATAAACTCTACCTCCAAATTTGATTGATGACGTCACTAAGAGGCTTT 745

RESULT 8

AAS56597
ID AAS56597 standard; cDNA; 2417 BP.

XX AAS56597;

XX 18-DEC-2001 (first entry)

XX Human cDNA for an ovarian cancer protein #221.

XX Human; sg; ovarian cancer protein; cancer; tumour; ovarian cancer;
XX endometrial cancer; cytostatic.

XX Homo sapiens.

XX WO200170976-A2.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US009062.

XX 21-MAR-2000; 2000US-0190710P.

XX 22-JUN-2000; 2000US-0213748P.

XX 19-DEC-2000; 2000US-0257276P.

XX (CORI-) CORIXA CORP.

XX Xu J, Pyle RA, Stolk JA;

XX WPI; 2001-607531/69.

XX Nucleic acids encoding 222 polypeptides associated with ovarian and
XX endometrial cancers, useful for diagnosing, preventing and treating
XX cancers.

XX Claim 1; Page 186-187; 187pp; English.

XX The invention relates to human polynucleotides encoding proteins
XX associated with ovarian and endometrial cancers. The polynucleotides and
XX the proteins they encode may be used in the prevention, diagnosis and
XX treatment of diseases associated with the inappropriate expression of
XX ovarian and endometrial cancer polypeptides (OECs). For example, the
XX polynucleotide (or an expression vector comprising the polynucleotide)
XX and the OEC may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of OECs by expressing inactive proteins or to
XX supplement the patients own production of them. Additionally, the
XX polynucleotide may be used to produce the OECs, by inserting the nucleic
XX acids into a host cell and culturing the cell to express the protein. The
XX polynucleotide and its complementary sequences may also be used as DNA
XX probes in diagnostic assays to detect and quantitate the presence of
XX similar nucleic acids in samples, and therefore which patients may be in
XX need of restorative therapy. The OECs may also be used as antigens in
XX the production of anti-OEC antibodies and in assays to identify
XX modulators of its expression and activity. The anti-OEC antibodies and
XX antagonists may also be used to down regulate expression and activity.
XX The anti-OEC antibodies may also be used as diagnostic agents for
XX detecting the presence of OECs in samples (e.g. by enzyme linked
XX immunosorbant assay (ELISA)) and hence diagnose patients with cancers.
XX The present sequence is a ovarian and endometrial cancer linked cDNA of
XX the invention

SQ Sequence. 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 4; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.7e-221;

Matches	709;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	ATGTGGGCAATTAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCGCGCGGAAGCC	60						
Db	36	ATGTGGGCAATTAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCGCGCGGAAGCC	95						
QY	61	ACCGCTGCGGTGATTTTCTCGCATGGATTGGGAGATACTGGGCACGCGATGGGCAGAGCC	120						
Db	96	ACCGCTGCGGTGATTTTCTCGCATGGATTGGGAGATACTGGGCACGCGATGGGCAGAGCC	155						
QY	121	TTTGCAGGTATCAGAGTTTCAATATATATCTGCCCGCATCGCTGTAGGCTT	180						
Db	156	TTTGCAGGTATCAGAGTTTCAATATATATCTGCCCGCATCGCTGTAGGCTT	215						
QY	181	GTTACATTAATATGAACGTGCTATGCCCTTCATGTTTGATATATTGGGCTTTTCACCA	240						
Db	216	GTTACATTAATATGAACGTGCTATGCCCTTCATGTTTGATATATTGGGCTTTTCACCA	275						
QY	241	GATTACAGGAGTGAATCTGGGATTAACAGGCAGCAGAAAATATAAAGCTTTGATT	300						
Db	276	GATTACAGGAGTGAATCTGGGATTAACAGGCAGCAGAAAATATAAAGCTTTGATT	335						
QY	301	GATCAAGAGTGAAGATGCGCATTCCTTCAACAGAAATATTTTGGAGGGTTTCTCAG	360						
Db	336	GATCAAGAGTGAAGATGCGCATTCCTTCAACAGAAATATTTTGGAGGGTTTCTCAG	395						
QY	361	GGAGAGCTTTATCTTTATATCTGCTTACACAGCAGAAACTGGCAGTGTCACT	420						
Db	396	GGAGAGCTTTATCTTTATATCTGCTTACACAGCAGAAACTGGCAGTGTCACT	455						
QY	421	GCACCTGATGCTGCTTCCACTTCCAGTCCACGGGATTTGACCCCTTTGGTCCCTGTATG	540						
Db	516	ATFAGAGATATTTCTATTCTCCAGTGCACGGGATTTGACCCCTTTGGTCCCTGTATG	575						
QY	541	TTTGGTCTCTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCTATGACCTTTT	600						
Db	576	TTTGGTCTCTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCTATGACCTTTT	635						
QY	601	AAAACTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAAGCAA	660						
Db	636	AAAACTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAAGCAA	695						
QY	661	TTTATTGATAAACTCTTACCTCCAAATTTGATTGACGTCACTAAGAGGCTTT	710						
Db	696	TTTATTGATAAACTCTTACCTCCAAATTTGATTGACGTCACTAAGAGGCTTT	745						

RESULT 9
ID ABK37030
XX ABK37030 standard; cdNA; 2417 BP.
XX AC ABK37030;
XX XX
XX DT 08-MAY-2002 (first entry)
XX XX
XX DE DNA encoding human lysophospholipase I #1.
XX KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
KW antiinflammatory; antiarteriosclerotic; vasotropic;
KW antilipidemia; cardiant; lysophospholipase I; inflammation; ischaemia;
KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
KW antisense gene therapy; gene; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200210185-A1.
XX XX
XX PD 07-FEB-2002.
XX XX
XX PF 20-JUL-2001; 2001WO-US022975.

XX	31-JUL-2000; 2000US-00629645.
PR	(ISIS-) ISIS PHARM INC.
PA	Bennett CF, Wyatt JR;
XX	WPI; 2002-188720/24.
XX	P-PSDB; AAU85132.
XX	Novel antisense compound useful for treating inflammation, hyperlipidemia, and cardiovascular disorders such as atherosclerosis and myocardial ischemia, inhibits lysophospholipase I.
XX	Example 13; Page 88-90; 131pp; English.
XX	The invention relates to an antisense compound (I) 8-30 nucleobases in length targeted to a nucleic acid molecule encoding lysophospholipase I (II), where (I) specifically hybridizes with and inhibits the expression of (II). (I) is useful for inhibiting the expression of (II) in cells or tissues, and for treating a human having a disease or condition associated with lysophospholipase I e.g. inflammation, hyperlipidaemia, and cardiovascular disorders such as atherosclerosis and myocardial ischaemia. (II) is useful as research reagent and diagnostics. (I) is also useful for distinguishing functions of various members of a biological pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
XX	represent lysophospholipase I coding sequences, antisense oligonucleotides and related PCR primers of the invention
XX	Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 U; 0 Other;
QY	Query Match 99.8%; Score 708.4; DB 6; Length 2417;
Db	Best Local Similarity 99.9%; Pred. No. 1.7e-221;
QY	Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1	ATGTGGGCAATTAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCGCGGAAGCC 60
36	ATGTGGGCAATTAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCGCGGAAGCC 95
61	ACCGCTGCGGTGATTTTCTCGCATGGATTGGGAGATACTGGGCACGCGATGGGCAGAGCC 120
96	ACCGCTGCGGTGATTTTCTCGCATGGATTGGGAGATACTGGGCACGCGATGGGCAGAGCC 155
121	TTTGCAGGTATCAGAGTTTCAATATATATCTGCCCGCATCGCTGTAGGCTT 180
156	TTTGCAGGTATCAGAGTTTCAATATATATCTGCCCGCATCGCTGTAGGCTT 215
181	GTTACATTAATATGAACGTGCTATGCCCTTCATGTTTGATATATTGGGCTTTTCACCA 240
216	GTTACATTAATATGAACGTGCTATGCCCTTCATGTTTGATATATTGGGCTTTTCACCA 275
241	GATTACAGGAGTGAATCTGGGATTAACAGGCAGCAGAAAATATAAAGCTTTGATT 300
276	GATTACAGGAGTGAATCTGGGATTAACAGGCAGCAGAAAATATAAAGCTTTGATT 335
301	GATCAAGAGTGAAGATGCGCATTCCTTCAACAGAAATATTTTGGAGGGTTTCTCAG 360
336	GATCAAGAGTGAAGATGCGCATTCCTTCAACAGAAATATTTTGGAGGGTTTCTCAG 395
361	GGAGAGCTTTATCTTTATATCTGCTTACACAGCAGAAACTGGCAGTGTCACT 420
396	GGAGAGCTTTATCTTTATATCTGCTTACACAGCAGAAACTGGCAGTGTCACT 455
421	GCACCTGATGCTGCTTCCACTTCCAGTCCACGGGATTTGACCCCTTTGGTCCCTGTATG 480
456	GCACCTGATGCTTCTATTCTCCAGTGCACGGGATTTGACCCCTTTGGTCCCTGTATG 515
481	ATFAGAGATATTTCTATTCTCCAGTGCACGGGATTTGACCCCTTTGGTCCCTGTATG 540
516	ATFAGAGATATTTCTATTCTCCAGTGCACGGGATTTGACCCCTTTGGTCCCTGTATG 575
541	TTTGGTCTCTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCTATGACCTTTT 600
576	TTTGGTCTCTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCTATGACCTTTT 635
601	AAAACTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAAGCAA 660
636	AAAACTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAAGCAA 695
661	TTTATTGATAAACTCTTACCTCCAAATTTGATTGACGTCACTAAGAGGCTTT 710
696	TTTATTGATAAACTCTTACCTCCAAATTTGATTGACGTCACTAAGAGGCTTT 745

prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 U; 0 Other;

Query Match	99.8%;	Score	708.4;	DB	13;	Length	2417;
Best Local Similarity	99.9%;	Pred. No.	1.7e-221;				
Matches	709;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
1	ATGTCGGGCAATAACATGTCAACCCCGGTGCCCGCATCGTGC CGCGCCCGCGAAGGCC	60					
36	ATGTCGGGCAATAACATGTCAACCCCGGTGCCCGCATCGTGC CGCGCCCGCGAAGGCC	95					
61	ACCGTGGCGGTGATTTTCTGTCATGGATTGGAGATACCTGGGCACGGATGGCAGAAAGCC	120					
96	ACCGTGGCGGTGATTTTCTGTCATGGATTGGAGATACCTGGGCACGGATGGCAGAAAGCC	155					
121	TTTGCAGGTATCAGAAAGTTACATATCAAAATATATCTGCCCGCATCGCGCTGTTAGGCT	180					
156	TTTGCAGGTATCAGAAAGTTACATATCAAAATATATCTGCCCGCATCGCGCTGTTAGGCT	215					
181	GTTACATTAATATGAACGTGGCTATGCTTCATGGTTTGATATATTATTTGGGCTTTTCACCA	240					
216	GTTACATTAATATGAACGTGGCTATGCTTCATGGTTTGATATATTATTTGGGCTTTTCACCA	275					
241	GATTCACAGGAGATGATCTGGGATTAACAGGCAGCAGAGAAATATAAAGCTTTTGATT	300					
276	GATTCACAGGAGATGAAATCTGGGATTAACAGGCAGCAGAGAAATATAAAGCTTTTGATT	335					
301	GATCAAGAAGTCAAGAAATGGCATTCCTTCTAAACAGAAATATTATTGGGAGGGTTTTCTCAG	360					
336	GATCAAGAAGTCAAGAAATGGCATTCCTTCTAAACAGAAATATTATTGGGAGGGTTTTCTCAG	395					
361	GGAGGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAAACTGGCAGGTCTCACT	420					
396	GGAGGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAAACTGGCAGGTCTCACT	455					
421	GCACCTCAGTTGCTGGCTCCACCTCTGGGCTTCCTTCCACAGGGTCTTATCGGTGGTGTCT	480					
456	GCACCTCAGTTGCTGGCTTCACCTTCGGGCTTCTTTCCACAGGGTCTTATCGGTGGTGTCT	515					
481	AATAGAGATATTTCTATTCTCCAGTSCCACGGGATTTGTGACCCCTTTGGTTCCTCCCTGATG	540					
516	AATAGAGATATTTCTATTCTCCAGTSCCACGGGATTTGTGACCCCTTTGGTTCCTCCCTGATG	575					
541	TTTGGTTCCTTACCGGTGAAAAATCAAAAAATTTGGTGAATTCACGCCAATCTGACCTTTT	600					
576	TTTGGTTCCTTACCGGTGAAAAATCAAAAAATTTGGTGAATTCACGCCAATCTGACCTTTT	635					

Query Match 99.8%; Score 708.4; DB 13; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.7e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGGCGGAATAACATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCCCGCGGAAGGCC 60
DB 36 ATGTGGCGGAATAACATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCCCGCGGAAGGCC 95

QY 61 ACCGCTGCGGTGATTTCTCTGATGATTTGGGAGATCTGGGCACGCGATGGGCAGGAAGCC 120
DB 96 ACCGCTGCGGTGATTTCTCTGATGATTTGGGAGATCTGGGCACGCGATGGGCAGGAAGCC 155

QY 121 TTTCAGAGTATCAGAAATTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 180
DB 156 TTTCAGAGTATCAGAAATTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 215

QY 181 GTTACATTAATAATGAAAGTGGCTTACCTTCATGTTTGTATATTTGGGCTTTTACCA 240
DB 216 GTTACATTAATAATGAAAGTGGCTTACCTTCATGTTTGTATATTTGGGCTTTTACCA 275

QY 241 GATTCACAGGAGTGAATCTGGATTAAACAGGCAGAGAAATATAAAGCTTTGATT 300
DB 276 GATTCACAGGAGTGAATCTGGATTAAACAGGCAGAGAAATATAAAGCTTTGATT 335

QY 301 GATCAAGAGTGAAGATGGCATTCCTCTAACAGAAATTAATTTGGGAGGGTTTCTCAG 360
DB 336 GATCAAGAGTGAAGATGGCATTCCTCTAACAGAAATTAATTTGGGAGGGTTTCTCAG 395

QY 361 GGAGGAGCTTTATCTTTTATATCTGCTTACACAGAGAAATCGGAGGTGTCAT 420
DB 396 GGAGGAGCTTTATCTTTTATATCTGCTTACACAGAGAAATCGGAGGTGTCAT 455

QY 421 GCACCTAGTGTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTCT 480
DB 456 GCACCTAGTGTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTCT 515

QY 481 AATAGAGATATTCTATTCTCCAGTCCACGGGGATTGTACCCCTTTGGTTCCCTCGATG 540
DB 516 AATAGAGATATTCTATTCTCCAGTCCACGGGGATTGTACCCCTTTGGTTCCCTCGATG 575

QY 541 TTGTGTTCTTTACGGTGAAAAAATAAATAAATGTTGGTGAATCCAGCCAAATGACCTTT 600
DB 576 TTGTGTTCTTTACGGTGAAAAAATAAATAAATGTTGGTGAATCCAGCCAAATGACCTTT 635

QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTCTCAACAGGAATGATGGATGTCAAGCAA 660
DB 636 AAAACCTATGAAGGTATGATGACAGTTCGTCTCAACAGGAATGATGGATGTCAAGCAA 695

QY 661 TTCAATTGATAAACTCCTACTCCTCAATTGATTGACGTCACTAAGAGGCCTT 710
DB 696 TTCAATTGATAAACTCCTACTCCTCAATTGATTGACGTCACTAAGAGGCCTT 745

RESULT 14

AAC98208
ID AAC98208 standard; cDNA; 2493 BP.
XX AC AAC98208;
XX AC AAC98208;
DT 09-MAR-2001 (first entry)
XX DE Human colon cancer antigen nucleotide sequence SEQ ID NO:218.
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
KW KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW KW neural disorder; immune system disorder; muscular disorder;
KW KW reproductive disorder; gastrointestinal disorder; renal disorder;
XX KW infectious disease; cardiovascular disorder; ss.
OS Homo sapiens.
XX

PN WO200055351-A1.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005883.
XX 12-MAR-1999; 99US-0124270P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
PI WPI; 2000-587534/55.
XX P-PSDB; AAB53451.
XX Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
PS Claim 1; Page 641; 2104pp; English.
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 2493 BP; 766 A; 442 C; 449 G; 836 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 3; Length 2493;
Best Local Similarity 99.9%; Pred. No. 1.7e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGGCGGAATAACATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCCCGCGGAAGGCC 60
DB 100 ATGTGGCGGAATAACATGTCAACCCCGCTGCCGCCATCGTGCCTCCGCCCGCGGAAGGCC 159

QY 61 ACCGCTGCGGTGATTTCTCTGATGATTTGGGAGATCTGGGCACGCGATGGGCAGGAAGCC 120
DB 160 ACCGCTGCGGTGATTTCTCTGATGATTTGGGAGATCTGGGCACGCGATGGGCAGGAAGCC 219

QY 121 TTTCAGAGTATCAGAAATTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 180
DB 220 TTTCAGAGTATCAGAAATTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 279

QY 181 GTTACATTAATAATGAAAGTGGCTTCAATGTTTGTATATTTGGGCTTTTACCCA 240
DB 280 GTTACATTAATAATGAAAGTGGCTTCAATGTTTGTATATTTGGGCTTTTACCCA 339

QY 241 GATTCACAGGAGTGAATCTGGGATTAACAGGCAGCAGAAATATAAAGCTTTGATT 300
DB 340 GATTCACAGGAGTGAATCTGGGATTAACAGGCAGCAGAAATATAAAGCTTTGATT 399

QY 301 GATCAAGAGTGAAGATGGCATTCCTCTAACAGAAATTAATTTGGGAGGGTTTCTCAG 360
DB 400 GATCAAGAGTGAAGATGGCATTCCTCTAACAGAAATTAATTTGGGAGGGTTTCTCAG 459

QY 361 GGAGGAGCTTTTATCTTTTATATCTGCTTACACAGAGAAATCGGAGGTGTCAT 420
DB 460 GGAGGAGCTTTTATCTTTTATATCTGCTTACACAGAGAAATCGGAGGTGTCAT 519

QY 421 GCACCTAGTGTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTCT 480

Db 520 GCACCTAGTGTGGCTTCCACTTGGGGTTCCTTTCCACAGGTCCTATTCGGTGTCT 579
Qy 481 AATAGAGATATTTCTATCTCCAGTGCACGGGGATTGTGACCTTTTGGTTCCCTGTGATG 540
Db 580 AATAGAGATATTTCTATCTCCAGTGCACGGGGATTGTGACCTTTTGGTTCCCTGTGATG 639
Qy 541 TTTGGTTCCTTACGGTGAAGAACTTAAACCAATTGGTGAATCCAGCCAAATGTGACCTTT 600
Db 640 TTTGGTTCCTTACGGTGAAGAACTTAAACCAATTGGTGAATCCAGCCAAATGTGACCTTT 699
Qy 601 AAACCTATGAGGTATGATGACAGTTCGTGTCAACAGGAATGATGATGTCAGCA 660
Db 700 AAACCTATGAGGTATGATGACAGTTCGTGTCAACAGGAATGATGATGTCAGCA 759
Qy 661 TTCAATTGATAAACTCCTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 710
Db 760 TTCAATTGATAAACTCCTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 809

RESULT 15

ACN38804
ID ACN38804 standard; cDNA; 2578 BP.
AC AC
XX ACN38804;
XX
DT 18-NOV-2004 (first entry)
XX

DE Tumour-associated antigenic target (TAT) cDNA DNAS25098, SEQ ID NO:2550.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX
XX Homo sapiens.

XX WO2004030615-A2.
XX
XX 15-APR-2004.
XX

XX 29-SEP-2003; 2003WO-US028547.
XX

XX 02-OCT-2002; 2002US-0414971P.
XX

XX (GETH) GENENTECH INC.
XX

XX Wu TD, Zhang Z, Zhou Y;
XX

XX WPI; 2004-347921/32.
XX

DR P-PSDB; ABM80990.
XX

XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX

XX Claim 1; SEQ ID NO 2550; 7273pp; English.
XX

XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful

CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX

XX Sequence 2578 BP; 766 A; 472 C; 498 G; 842 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 13; Length 2578;
Best Local Similarity 99.9%; Pred. No. 1.8e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTGCGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCCGGAAAGGCC 60
Db 195 ATGTGCGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCCCGGAAAGGCC 254
Qy 61 ACCGTGCGGTGATTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGGCAAGGCC 120
Db 255 ACCGTGCGGTGATTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGGCAAGGCC 314
Qy 121 TTTGAGGTATCAGAGTTTCAATATATCTGCCCGCATCGTCCCGCCCGGAAAGGCC 180
Db 315 TTTGAGGTATCAGAGTTTCAATATATCTGCCCGCATCGTCCCGCCCGGAAAGGCC 374
Qy 181 GTTACATTAATATGAACGTGCTATGCTTTCATGTTTGTATATTTGGGCTTTTCAACA 240
Db 375 GTTACATTAATATGAACGTGCTATGCTTTCATGTTTGTATATTTGGGCTTTTCAACA 434
Qy 241 GATTTCAGGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300
Db 435 GATTTCAGGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 494
Qy 301 GATCAGAGAGTGAAGTGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
Db 495 GATCAGAGAGTGAAGTGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 554
Qy 361 GGAGGAGCTTTTATCTTTTATATATCTGCTTACCACACAGCAAACTGGCAGGTGCT 420
Db 555 GGAGGAGCTTTTATCTTTATATATCTGCTTACCACACAGCAAACTGGCAGGTGCT 614
Qy 421 GCATCAGTGTGCTTCCATCTTGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 480
Db 615 GCATCAGTGTGCTTCCATCTTGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 674
Qy 481 AATAGAGATATTTCTATTTCTCCAGTGCACGGGATTGTGACCTTTTGGTTCCCTGATG 540
Db 675 AATAGAGATATTTCTATTTCTCCAGTGCACGGGATTGTGACCTTTTGGTTCCCTGATG 734
Qy 541 TTTGGTTCTTTACGGTGAAGAACTTAAAAACAATTGGTGAATCCAGCAATGTGACCTTT 600
Db 735 TTTGGTTCTTTACGGTGAAGAACTTAAAAACAATTGGTGAATCCAGCAATGTGACCTTT 794
Qy 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAATGATGATGTCAGCAA 660
Db 795 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAATGATGATGTCAGCAA 854
Qy 661 TTCAATTGATAAACTCCTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 710
Db 855 TTCAATTGATAAACTCCTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 904

Search completed: April 14, 2006, 14:01:06

Job time : 589 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:28:32 ; Search time 3943 Seconds

(without alignments)
8424.760 Million cell updates/sec

Title: US-09-493-601B-1

Perfect score: 710

Sequence: 1 atgtgcggcaataacatgtc.....tgacgtcactaagaggcctt 710

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_hic.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_est7.*
- 9: gb_gsl.*
- 10: gb_gsl2.*
- 11: gb_gsl3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708.4	99.8	725	8	CX752219 AGENCOURT
2	708.4	99.8	919	2	BG696407 602659503
3	708.4	99.8	1348	4	AF077198 Homo sapi
4	704.4	99.2	1042	3	BM558765 AGENCOURT
5	701	98.7	1061	3	BM475259 AGENCOURT
6	700.4	98.6	2476	4	CR858568 Pongo pyg
7	690.8	97.3	904	7	CN805809 ILLUMIN
8	690.6	97.3	774	1	AU133073 AU133073
9	679.4	95.7	711	3	BI550895 603195310
10	677.6	95.4	1088	3	BM465006 AGENCOURT
11	674.8	95.0	895	2	BG614082 602641734
12	673.2	94.8	889	3	BQ227373 AGENCOURT
13	670.4	94.4	691	3	BI906551 603064126
14	661.4	93.2	796	1	AU132495 AU132495
15	660.4	93.0	896	2	BG528464 602579913
16	659.8	92.9	709	2	BG501911 602548224
17	656.4	92.5	1050	2	BG166847 602345021
18	655.2	92.3	798	7	CF994968 AGENCOURT
19	650	91.5	803	5	BX366646 BX366646
20	648.4	91.3	898	2	BG613559 602641906
21	641.8	90.4	729	2	BG615693 602643058
22	640	90.1	765	2	BG722409 602693642

23	634	89.3	740	2	BG773497	BG773497 602720223
24	633.8	89.3	698	2	BG282835	BG282835 602405938
25	633.2	89.2	786	6	CB991804	CB991804 AGENCOURT
26	630	88.7	796	2	BE618034	BE618034 601462392
27	630	88.7	1161	3	BM457120	BM457120 AGENCOURT
28	629.8	88.7	838	1	AV757844	AV757844 AV757844
29	625.8	88.1	815	8	CX754949	CX754949 AGENCOURT
30	614.4	86.5	895	2	BF314398	BF314398 601901151
31	613	86.3	658	6	CD701760	CD701760 EST18284
32	609.4	85.8	931	2	CR750918	CR750918 DKF2P4590
33	609.4	85.8	931	2	BF970655	BF970655 60273811
34	605.8	85.3	853	3	BI549474	BI549474 603192140
35	605.6	85.3	725	3	BI596291	BI596291 603243007
36	602.4	84.8	1300	4	AF077199	AF077199 Homo sapi
37	592.4	83.4	640	2	BG545991	BG545991 602573290
38	591.2	83.3	825	2	BG721347	BG721347 602694890
39	590	83.1	777	7	CO738296	CO738296 S1LE04C20
40	585.8	82.5	613	2	BG389590	BG389590 602414316
41	585.8	82.5	734	2	BG433925	BG433925 602497218
42	585.2	82.4	728	7	CO561951	CO561951 AGENCOURT
43	584	82.3	821	5	BQ440078	BQ440078 AGENCOURT
44	583.2	82.1	739	7	CN408025	CN408025 170004277
45	580.4	81.7	926	5	BQ899917	BQ899917 AGENCOURT

ALIGNMENTS

RESULT 1
CX752219
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

725 bp mRNA linear EST 24-JAN-2005
CX752219 AGENCOURT_40989196 NIH_MGC_281 Homo sapiens CDNA clone
IMAGE:7783359 3', mRNA sequence.
CX752219
CX752219.1 GI:58048874
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 725)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
CDNA Library Preparation: Express Genomics
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15943 row: h column: 13
High quality sequence stop: 723.
Location/Qualifiers
1..725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7783359"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B TONa"
/clone_lib="NIH MGC 281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
EcoRV, Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-6, NIH Registry designation UC06. Positive for OCT4

expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence Passage 62. cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGAGCGCGGCC(7)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 2.0 kb. This primary library is normalized (non-normalized primary library is NIH-MGC 280) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match 99.8%; Score 708.4; DB 8; Length 725;
Best Local Similarity 99.9%; Pred. No. 3e-203;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAACATGTCACACCCGCTGCGCGGCATCGTCCCGCGCGCGCGAAGGCC 60
Db 8 ATGTGCGGCAATAACATGTCACACCCGCTGCGCGGCATCGTCCCGCGCGCGCGAAGGCC 67

QY 61 ACCGCTGCGGTGATTTCTGTCATGATGATTTGGAGATATCTGGCAGCGATGGCAGAGCC 120
Db 68 ACCGCTGCGGTGATTTCTGTCATGATGATTTGGAGATATCTGGCAGCGATGGCAGAGCC 127

QY 121 TTTGAGGTATCAGAGGTTTACATATCAATATATCTGCCCATCTGCCCATCTGTAGGCT 180
Db 128 TTTGAGGTATCAGAGGTTTACATATCAATATATCTGCCCATCTGCCCATCTGTAGGCT 187

QY 181 GTTACATTAATATGAACGTGCTATGCTTCATGTTTGTATATTTGGGCTTTTACCA 240
Db 188 GTTACATTAATATGAACGTGCTATGCTTCATGTTTGTATATTTGGGCTTTTACCA 247

QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGAT 300
Db 248 GATTCACAGGAGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGAT 307

QY 301 GATCAGAGTCAAGAGTGGCATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 360
Db 308 GATCAGAGTCAAGAGTGGCATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 367

QY 361 CGAGGAGCTTTATCTTTATATATGCTTCATGCTTACACAGAGAACTGCGAGGTGCT 420
Db 368 CGAGGAGCTTTATCTTTATATATGCTTCATGCTTACACAGAGAACTGCGAGGTGCT 427

QY 421 GCATCAGTGTGCTTCCATCTGCGGCTTCCCTTCCACAGAGTCTTATCGGTGCT 480
Db 428 GCATCAGTGTGCTTCCATCTGCGGCTTCCCTTCCACAGAGTCTTATCGGTGCT 487

QY 481 AATAGAGATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTGGTCCCTGATG 540
Db 488 AATAGAGATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTGGTCCCTGATG 547

QY 541 TTTGGTCTCTTACGGTGAAGAACTTAAACCAATGGTGAATCCAGCCTTGAACCTTT 600
Db 548 TTTGGTCTCTTACGGTGAAGAACTTAAACCAATGGTGAATCCAGCCTTGAACCTTT 607

QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAGCAA 660
Db 608 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAGCAA 667

QY 661 TTTCAATGATAAACTCTACCTCCATTTGATTCAGCTCACTAGAGGCCCTT 710
Db 668 TTTCAATGATAAACTCTACCTCCATTTGATTTGACGTCACTAGAGGCCCTT 717

RESULT 2
BG696407
LOCUS 919 bp mRNA linear EST 07-MAY-2001
DEFINITION 602659503F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4802665 5', mRNA sequence.
ACCESSION BG696407
VERSION BG696407.1 GI:13961520

KEYWORDS

SOURCE

ORGANISM

EST. Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 919)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10697 row: e column: 02

High quality sequence stop: 807.

Location/Qualifiers

1..919

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4802665"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

FEATURES

source

ORIGIN

Query Match 99.8%; Score 708.4; DB 2; Length 919;
Best Local Similarity 99.9%; Pred. No. 3.3e-203;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCATTAACATGTCACACCCGCTGCGCGCATGTCGCCCGCGCGCGCGAAGGCC 60
Db 27 ATGTGCGGCATTAACATGTCACACCCGCTGCGCGCATGTCGCCCGCGCGCGCGAAGGCC 86

QY 61 ACCGCTGCGGTGATTTCTGTCATGATGATTTGGAGATATCTGGCAGCGATGGCAGAGCC 120
Db 87 ACCGCTGCGGTGATTTCTGTCATGATGATTTGGAGATATCTGGCAGCGATGGCAGAGCC 146

QY 121 TTTGAGGTATCAGAGTTCATATFCAAAATATATCTGCCCGCATGCGCTGTAGGCT 180
Db 147 TTTGAGGTATCAGAGTTCATATFCAAAATATATCTGCCCGCATGCGCTGTAGGCT 206

QY 181 GTTACATTAATATGAACGTGCTATGCTTCATGTTTGTATATTTGGGCTTTTACCA 240
Db 207 GTTACATTAATATGAACGTGCTATGCTTCATGTTTGTATATTTGGGCTTTTACCA 266

QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGAT 300
Db 267 GATTCACAGGAGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGAT 326

QY 301 GATCAAGAGTGAAGAAATGGCAATCTCTTCTAAACAGAAATTTTGGAGGGTTTCTCAG 360
Db 327 GATCAAGAGTGAAGAAATGGCAATCTCTTCTAAACAGAAATTTTGGAGGGTTTCTCAG 386

QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAGAACTGCGAGGTGCT 420
Db 387 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAGAACTGCGAGGTGCT 446

QY 421 GCATCAGTGTGCTTCCACTTCCGGCTTCCCTTCCACAGGAGTCTTATCGGTGCT 480
Db 447 GCATCAGTGTGCTTCCACTTCCGGCTTCCCTTCCACAGGAGTCTTATCGGTGCT 506

QY 481 AATAGAGATATTTCTTATCTCAGTGCACGGGATTTGACCCCTTGGTTCCTCCTGATG 540

```
Db 507 AATAGAGATATTTCTTATTTCTCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATG 566
Qy 541 TTTGGTTCTCTTACGGTGGAAAAAATAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 600
Db 567 TTTGGTTCTCTTACGGTGGAAAAAATAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 626
Qy 601 AAAACCTATGAAGGTATGATGACACAGTTTGGTGTCAACAGGAATGATGATGTCAGCNA 660
Db 627 AAAACCTATGAAGGTATGATGACACAGTTTGGTGTCAACAGGAATGATGATGTCAGCNA 686
Qy 661 TTCAATTGATAAACTCTCACTCTCAATTTGATTCACAGTCACTAAGAGCCCTT 710
Db 687 TTCAATTGATAAACTCTCACTCTCAATTTGATTCACAGTCACTAAGAGCCCTT 736
```

RESULT 3

```
AF077198 1348 bp mRNA linear HTC 22-MAY-2001
LOCUS Homo sapiens lysophospholipase mRNA, complete cds.
```

DEFINITION

```
AF077198
```

ACCESSION

```
AF077198.1 GI:4679009
```

VERSION

```
HTC.
```

KEYWORDS

```
Homo sapiens (human)
```

SOURCE

```
Homo sapiens
```

ORGANISM

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```
Hominoidea; Homo.
```

```
1 (bases 1 to 1348)
```

```
Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G.,
```

```
Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,
```

```
Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.
```

```
Cloning and functional analysis of cDNAs with open reading frames
```

```
for 300 previously undefined genes expressed in CD34+ hematopoietic
```

```
stem/progenitor cells
```

```
Genome Res. 10 (10), 1546-1560 (2000)
```

```
11042152
```

```
2 (bases 1 to 1348)
```

```
Shen, Y., Guan, Z., Gu, J., Ye, M., Zhou, J., Zhang, Q., Xu, S., He, K.,
```

```
Chen, S., Mao, M. and Chen, Z.
```

```
Human lysophospholipase gene
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```
Unpublished
```

```
3 (bases 1 to 1348)
```

```
Shen, Y.
```

```
Direct Submission
```

```
Submitted (10-JUL-1998) Shanghai Institute of Hematology, Shanghai
```

```
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
```

```
Shanghai 200025, P. R. China
```

```
Location/Qualifiers
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1. .1348
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/cell_type="CD34+ cell"
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6. .698
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/codon_start=1
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/product="lysophospholipase"
```

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/protein_id="AA026933.1"
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/db_xref="GI:4679010"
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/translation="MCGNNMSTPLPAIVPAARKATRAVIFLHGLDGTGHGAEAPAGI
```

```
RSRHYKPCFAPVRPTLVNMMVPSWFDIIIGLSPDSQDESGIKQAAENIKALIDQ
```

```
EVNGKIPNRIILGFSQGGALSALTATTOQLAGVTALSCWLPRLRSPQPIGGA
```

```
NRDISTLOCHGDCDPLVPLMPGSLTVEKLTLVNPANVTFTKTYEGMWHSSCCQEMWDV
```

```
KQFDIKLLFPID"
```

CDS

```
/
```

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Query Match 99.8%; Score 708.4; DB 4; Length 1348;
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```
Best Local Similarity 99.9%; Pred. NO. 3.7e-203;
```

```
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

ORIGIN

```
1 ATGTGGCGCAATACATGTCAACCCCGCTGCCCGCCATCGTGCCTCCGCGCGCGGAGGCC 60
```

```
|||||
```

```
6 ATGTGGCGCAATACATGTCAACCCCGCTGCCCGCCATCGTGCCTCCGCGCGGAGGCC 65
```

```
Qy 61 ACCCTGCGGTGATTTTCTCCTCATGGATTGGAGATCTGGSCACGGATGGCAGAAGCC 120
Db 66 ACCCTGCGGTGATTTTCTCCTCATGGATTGGAGATCTGGSCACGGATGGCAGAAGCC 125
Qy 121 TTTGAGGTATCAGAAAGTTTCATATCAATATATCTGCCCGCATCGCCTGTGAGGCT 180
Db 126 TTTGAGGTATCAGAAAGTTTCATATCAATATATCTGCCCGCATCGCCTGTGAGGCT 185
Qy 181 GTTACATTAATAATGAAGTGGCTATGCTTTCATGTTTATATTTATTTGGGCTTTTCAACA 240
Db 186 GTTACATTAATAATGAAGTGGCTATGCTTTCATGTTTATATTTATTTGGGCTTTTCAACA 245
Qy 241 GATTCACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAAGCTTTGATT 300
Db 246 GATTCACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAAGCTTTGATT 305
Qy 301 GATCAAGAAGTGAAGATGGCATTCCTTCTTAACAGAAATATTTTGGGAGGGTTTCTCAG 360
Db 306 GATCAAGAAGTGAAGATGGCATTCCTTCTTAACAGAAATATTTTGGGAGGGTTTCTCAG 365
Qy 361 GGAGAGGCTTATCTTTATATATCTGCTTACCTTACACAGCAGAGAAATGTCAGTGTCACT 420
Db 366 GGAGAGGCTTATCTTTATATATCTGCTTACCTTACACAGCAGAGAAATGTCAGTGTCACT 425
Qy 421 GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGTGCT 480
Db 426 GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGTGCT 485
Qy 481 AATAGAGATATTTCTTATTTCTCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATG 540
Db 486 AATAGAGATATTTCTTATTTCTCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATG 545
Qy 541 TTTGGTTCTCTTACGGTGGAAAAAATAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 600
Db 546 TTTGGTTCTCTTACGGTGGAAAAAATAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 605
Qy 601 AAAACCTATGAAGGTATGATGACACAGTTTGGTGTCAACAGGAATGATGATGTCAGCA 660
Db 606 AAAACCTATGAAGGTATGATGACACAGTTTGGTGTCAACAGGAATGATGATGTCAGCA 665
Qy 661 TTCAATTGATAAACTCTCACTCTCAATTTGATTCACAGTCACTAAGAGCCCTT 710
Db 666 TTCAATTGATAAACTCTCACTCTCAATTTGATTCACAGTCACTAAGAGCCCTT 715
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RESULT 4

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BM558765
```

```
LOCUS
```

```
DEFINITION
```

```
5', mRNA sequence.
```

```
ACCESSION
```

```
BM558765
```

```
VERSION
```

```
BM558765.1 GI:18801785
```

```
KEYWORDS
```

```
EST.
```

```
SOURCE
```

```
Homo sapiens (human)
```

```
Homo sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```
Hominoidea; Homo.
```

```
1 (bases 1 to 1042)
```

```
NIH-MGC http://mgc.nci.nih.gov/
```

```
National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
Unpublished (1999)
```

```
Contact: Robert Strausberg, Ph.D.
```

```
Email: cgabbs-r@mail.nih.gov
```

```
Tissue Procurement: ATCC
```

```
CDNA Library Preparation: Life Technologies, Inc.
```

```
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

```
DNA Sequencing by: Agencourt Bioscience Corporation
```

```
Clone distribution: MGC clone distribution information can be
```

```
found through the I.M.A.G.E. Consortium/LLNL at:
```

```
http://image.llnl.gov
```

```
Plate: LLAM12264 row: b column: 18
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```
High quality sequence stop: 680.
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FEATURES
source

Location/Qualifiers
1. .1042
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:551025"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 99.2%; Score 704.4; DB 3; Length 1042;
Best Local Similarity 99.7%; Pred. No. 5.5e-202;
Matches 705; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCGGCAATTAACATGTCACCCCGCTGCCCGCATCGTCCCGCGCCGCGAAGGCCACC 63
Db |||||||
1 TCGGCAATTAACATGTCACCCCGCTGCCCGCATCGTCCCGCGCCGCGAAGGCCACC 60
QY 64 GCTGCGGTGATTTCTCGTCATGGATTGGGAGATACCTGGGCACCGATGGGCAGAACCTTT 123
Db |||||||
61 GCTGCGGTGATTTCTCGTCATGGATTGGGAGATACCTGGGCACCGATGGGCAGAACCTTT 120
QY 124 CGAGGTATCAGAAGTTTCACATATCAAAATATATCTGCCCGCATCGGCTGTAGGCGCTGT 183
Db |||||||
121 CGAGGTATCAGAAGTTTCACATATCAAAATATATCTGCCCGCATCGGCTGTAGGCGCTGT 180
QY 184 ACATTAATATGAAGTGGCTATGCCCTCATGTTTGAATATTATTTGGGCTTTTCCACAGAT 243
Db |||||||
181 ACATTAATATGAAGTGGCTATGCCCTCATGTTTGAATATTATTTGGGCTTTTCCACAGAT 240
QY 244 TCACAGGAGGATGAATCTGGGATTAAACAGGACGACAGAAAATATAAAAGCTTTTGATTGAT 303
Db |||||||
241 TCACAGGAGGATGAATCTGGGATTAAACAGGACGACAGAAAATATAAAAGCTTTTGATTGAT 300
QY 304 CAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGGAGGTTTCTCAGGGA 363
Db |||||||
301 CAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGGAGGTTTCTCAGGGA 360
QY 364 GGAGCTTTATCTTTATATCTGCCCTTACACAGCAGAAACTGCGAGTGTCACTGCA 423
Db |||||||
361 GGAGCTTTATCTTTATATCTGCCCTTACACAGCAGAAACTGCGAGTGTCACTGCA 420
QY 424 CTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGTAAAT 483
Db |||||||
421 CTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGTAAAT 480
QY 484 AGAGATATTTCTATTTCTCAGTGCACGGGGATTGACCCCTTGGTTCCCTGATGTTT 543
Db |||||||
481 AGAGATATTTCTATTTCTCAGTGCACGGGGATTGACCCCTTGGTTCCCTGATGTTT 540
QY 544 GGTCTCTTACGGTGGAAAACCTAAACATTTGGTGAATCCAGCCAACTGACCTTTAA 603
Db |||||||
541 GGTCTCTTACGGTGGAAAACCTAAACATTTGGTGAATCCAGCCAACTGACCTTTAA 600
QY 604 ACCATGAAGGTATGATGCACAGTTCGTCTCAACAGGAAATGATGGATGTCAAGCAATTC 663
Db |||||||
601 ACCATGAAGGTATGATGCACAGTTCGTCTCAACAGGAAATGATGGATGTCAAGCAATTC 660
QY 664 ATTGATAAACTCCTACCTCAATTTGATTCAGTCACTAAGAGGCTTT 710
Db |||||||
661 ATTGATAAACTCCTACCTCAATTTGATTCAGTCACTAAGAGGCTTT 707

RESULT 5
BM475259
LOCUS
DEFINITION 6477939 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5578672
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM475259
BM475259.1 GI:18524301
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1061)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12334 row: b column: 17
High quality sequence stop: 618.
Location/Qualifiers
1. .1061
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5578672"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

FEATURES
source

Location/Qualifiers
1. .1061
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5578672"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 98.7%; Score 701; DB 3; Length 1061;
Best Local Similarity 99.2%; Pred. No. 6e-201;
Matches 704; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGTCGGCAATAACATGTCACCCCGCTGCCCGCATCGTCCCGCGCCGCGAAGGCC 60
Db |||||||
17 ATGTCGGCAATAACATGTCACCCCGCTGCCCGCATCGTCCCGCGCCGCGAAGGCC 76
QY 61 ACCGCTGGGTGATTTTCTGTCATGGATTGGGAGATACCTGGGCACGGATGGGCAGAGCC 120
Db |||||||
77 ACCGCTGGGTGATTTTCTGTCATGGATTGGGAGATACCTGGGCACGGATGGGCAGAGCC 136
QY 121 TTTGAGGTATCAGAAATTCACATATCAAAATATATCTGCCCGCATCGGCTGTAGGCT 180
Db |||||||
137 TTTGAGGTATCAGAAATTCACATATCAAAATATATCTGCCCGCATCGGCTGTAGGCT 196
QY 181 GTTACATTAATAATGAACGTGCTATGCTTCATGTTTGAATATTATTTGGGTTTCAACA 240
Db |||||||
197 GTTACATTAATAATGAACGTGCTATGCTTCATGTTTGAATATTATTTGGGTTTCAACA 256
QY 241 GATTACAGGAGGATGAATCTGGGATTAACAGGACGACGAGAAAATATAAAAGCTTTGATT 300
Db |||||||
257 GATTACAGGAGGATGAATCTGGGATTAACAGGACGACGAGAAAATATAAAAGCTTTGATT 316
QY 301 GATCAAGAGTCAAGATGGCATTCCTCTTAACAGAAATTTATTTTGGAGGGTTTCTCAG 360
Db |||||||
317 GATCAAGAGTCAAGATGGCATTCCTCTTAACAGAAATTTATTTTGGAGGGTTTCTCAG 376
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCCCTTACCAACAGCAAGAACTGGCAGGTGTCACT 420
Db |||||||
377 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCAACAGCAAGAACTGGCAGGTGTCACT 436
QY 421 GCATCTCAGTTGCTGGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTATCGGTGGTGT 480
Db |||||||
437 GCATCTCAGTTGCTGGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTATCGGTGGTGT 496

QY 481 AATAGAGATATTCTTCTCCAGTGCACCGGGATTTGTGACCCCTTTGGTTCCTCCCTGATG 540
|||||
Db 497 AATAGAGATATTCTTATTCTCCAGTGCACCGGGATTTGTGACCCCTTTGGTTCCTCCCTGATG 556
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QY 541 TTTGGTCTCTTACCGTGAAAAAATAAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
|||||
Db 557 TTTGGTCTCTTACCGTGAAAAAATAAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 616
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QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGCAAAATGATGATGTCAGCA 660
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Db 617 ANAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGCAAAATGATGATGTCAGCA 676
|||||
QY 661 TTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTAAGAGGCCCTT 710
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Db 677 TTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTAAGAGGCCCTT 726
|||||

RESULT 6
LOCUS CR858568 2476 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cdna DKFp45900134 (from clone DKFp45900134).
ACCESSION CR858568
VERSION CR858568.1 GI:55728082

KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.

REFERENCE 1 (bases 1 to 2476)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Wewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wienann,S.

CONSTRM The German CDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY

COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKFp45900134) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=DKFp45900134

Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
1..2476
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFp45900134"
/tissue_type="cortex"
/clone_lib="459 (synonym: pcor1). Vector pSport1_sfi; host
DH10B; sites SfiIa + SfiIb"
/dev_stage="adult"
/notes="lysophospholipase I (Homo sapiens)"
1..2476
/gene="DKFp45900134"
76..768
/gene="DKFp45900134"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAH90793.1"
/db_xref="GI:55728083"
/translation="MCGNNMSTPLPAIIPAARKATAAVIFLHGLGDTGHGWAFAFAGI
RSHIKYICPHAPVRVTLMNAMPWFEDILGLSPDSOEDSGIKQAAENIKALIDQ
EVANGIPSNRIILGGFSQGLASLYLTALTITQKLAGVTALSCWLPILASFPOGPFIGGA
NRDITSLCHGDGDCDPLVPLMFGSLTVEKLKTLVNPANVTFTKYEGBMHSSCCQEMMDV
KQFIDKLPLPID"

FEATURES
Source

gene
CDS

ORIGIN

Query Match 98.6%; Score 700.4; DB 4; Length 2476;
Best Local Similarity 99.2%; Pred. No. 1.2e-200;
Matches 704; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGTCGGCAATAACATGTCAACCGCTGCCCGCATCTGTCGCCCGCCCGCGAAGGCC 60
|||||
Db 76 ATGTCGGCAATAACATGTCAACCGCTGCCCGCATCTGTCGCCCGCCCGCGAAGGCC 135
|||||
QY 61 ACCGCTCGGGTGATTTCTCTCATGGATTGGGAGATCTGGGCAACGATGGGCAAGGCC 120
|||||
Db 136 ACCGCTCGGGTGATTTCTCTCATGGATTGGGAGATCTGGGCAACGATGGGCAAGGCC 195
|||||
QY 121 TTTGAGGTATCAGAAAGTTTCAATATATATCTGCCCGCATCTGTCGCCCGCTTTAGGCC 180
|||||
Db 196 TTTGAGGTATCAGAAAGTTTCAATATATATCTGCCCGCATCTGTCGCCCGCTTTAGGCC 255
|||||
QY 181 GTTACATTAAATATGAACTGCTTCTCATGGTTTGATTTATTTGGGGCTTTTCCACCA 240
|||||
Db 236 GTTACATTAAATATGAACTGCTTCTCATGGTTTGATTTATTTGGGGCTTTTCCACCA 315
|||||
QY 241 GATTCACAGGAGGATGAATCTGGGATTAAACAGGAGCAGAGAAAATATAAAAGCTTTGAT 300
|||||
Db 316 GATTCACAGGAGGATGAATCTGGGATTAAACAGGAGCAGAGAAAATATAAAAGCTTTGAT 375
|||||
QY 301 GATCAAGAGTGAAGATGGGATTTCTTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 360
|||||
Db 376 GATCAAGAGTGAAGATGGGATTTCTTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 435
|||||
QY 361 GGAGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGCAAACTGGCAGGTGTCAC 420
|||||
Db 436 GGAGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGCAAACTGGCAGGTGTCAC 495
|||||
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTATTCGGTGTGCT 480
|||||
Db 496 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTATTCGGTGTGCT 555
|||||
QY 481 AATAGATATTTCTTATTTCTCAGTGCACGGGGATTTGACCCCTTTGGTTCCTCCCTGATG 540
|||||
Db 556 AATAGATATTTCTTATTTCTCAGTGCACGGGGATTTGACCCCTTTAGTTCCTCCCTGATG 615
|||||
QY 541 TTTGGTCTCTTACCGTGAAAAAATAAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
|||||
Db 616 TTTGGTCTCTTACCGTGAAAAAATAAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 675
|||||
QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGCAAAATGATGATGTCAGCAA 660
|||||
Db 676 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGCAAAATGATGATGTCAGCAA 735
|||||
QY 661 TTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTAAGAGGCCCTT 710
|||||
Db 736 TTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTAAGAGGCCCTT 785
|||||

RESULT 7
LOCUS CN805809 904 bp mRNA linear EST 26-MAY-2004
DEFINITION ILLUMIGEN MCQ 5802 Katze MMR Macaca mulatta cDNA clone IBIUW:14245
5' similar to "Bases 1 to 814 highly similar to human LYPLA1
(Hs.446676), mRNA sequence.
CN805809
CN805809.1 GI:47701785
EST.
Macaca mulatta (rhesus monkey)
Macaca mulatta

ACCESSION CN805809
VERSION CN805809.1
KEYWORDS EST.
SOURCE Macaca mulatta

ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
1 (bases 1 to 904)

REFERENCE 1 (bases 1 to 904)
AUTHORS Magnus,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agui,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.

TITLE Analysis of the Macaca mulatta transcriptome and the sequence

JOURNAL
PUBMED
COMMENT

divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15998449
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.06. 738 Q20 bases.
PCR Primers
FORWARD: CCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGCAATGGGTA
Insert Length: 904 Std Error: 0.00
Plate: CL000044 row: A column: 10
Seq primer: CCTCACTAAAGGGAACAAA
POLYA=Yes.

Location/Qualifiers
1..904
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUV:14245"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="katze_MBR"

/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

FEATURES
source

Query Match
Best Local Similarity 98.3%; Pred. No. 7.1e-198;
Matches 698; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATTAACATGTCACACCCCGCTGCCGCCATCGTCCCGCCCGCGGGAAGGCC 60
DB 5 ATGTGGGCAATTAACATGTCACACCCCGCTGCCGCCATCGTCCCGCCCGCGGGAAGGCC 64
QY 61 ACCGCTCGCGTGAATTTCTGATGATGGAGATGATGCGACGCGATGGCGCAGAGGCC 120
DB 65 ACCGCTCGCGTGAATTTCTGATGATGGAGATGATGCGACGCGATGGCGCAGAGGCC 124
QY 121 TTTCAGAGTATCAGAGTTTCATATCAATATATCTGCCCGATGCGCTGTAGGCCT 180
DB 125 TTTCAGAGTATCAGAGTTTCATATCAATATATCTGCCCGATGCGCTGTAGGCCT 184
QY 181 GTTACATTAATATGAACGTGCTATGCTTCATGTTTATATTTGGGCTTTTCACCA 240
DB 185 GTTACATTAATATGAACGTGCTATGCTTCATGTTTATATTTGGGCTTTTCACCA 244
QY 241 GATTCACAGAGATGAATCTGGGATTAACAGGACGACAGAAAATATAAAGCTTTGATT 300
DB 245 GATTCACAGAGATGAATCTGGGATTAACAGGACGACAGAAAATATAAAGCTTTGATT 304
QY 301 GATCAAGAGTGAAGATGGCAATCTCTCTAACAAGATTTATTTGGAGGGTTTCTCAG 360
DB 305 GATCAAGAGTGAAGATGGCAATCTCTCTAACAAGATTTATTTGGAGGGTTTCTCAG 364
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTACACAGCAGAACTGCGAGTGTCACT 420
DB 365 GGAGGAGCTTTATCTTTATATCTGCTTACACAGCAGAACTGCGAGTGTCACT 424
QY 421 GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGTCT 480
DB 425 GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGTCT 484
QY 481 AATAGAGATATTCTATTCTCCAGTCCACAGGGATTTGACCCCTTTGGTTCCCTGTATG 540
DB 485 AATAGAGATATTCTATTCTCCAGTCCACAGGGATTTGACCCCTTTAGTTCCCTGTATG 544

ORIGIN

Query Match 97.3%; Score 690.8; DB 7; Length 904;
Best Local Similarity 98.3%; Pred. No. 7.1e-198;
Matches 698; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATTAACATGTCACACCCCGCTGCCGCCATCGTCCCGCCCGCGGGAAGGCC 60
DB 5 ATGTGGGCAATTAACATGTCACACCCCGCTGCCGCCATCGTCCCGCCCGCGGGAAGGCC 64
QY 61 ACCGCTCGCGTGAATTTCTGATGATGGAGATGATGCGACGCGATGGCGCAGAGGCC 120
DB 65 ACCGCTCGCGTGAATTTCTGATGATGGAGATGATGCGACGCGATGGCGCAGAGGCC 124
QY 121 TTTCAGAGTATCAGAGTTTCATATCAATATATCTGCCCGATGCGCTGTAGGCCT 180
DB 125 TTTCAGAGTATCAGAGTTTCATATCAATATATCTGCCCGATGCGCTGTAGGCCT 184
QY 181 GTTACATTAATATGAACGTGCTATGCTTCATGTTTATATTTGGGCTTTTCACCA 240
DB 185 GTTACATTAATATGAACGTGCTATGCTTCATGTTTATATTTGGGCTTTTCACCA 244
QY 241 GATTCACAGAGATGAATCTGGGATTAACAGGACGACAGAAAATATAAAGCTTTGATT 300
DB 245 GATTCACAGAGATGAATCTGGGATTAACAGGACGACAGAAAATATAAAGCTTTGATT 304
QY 301 GATCAAGAGTGAAGATGGCAATCTCTCTAACAAGATTTATTTGGAGGGTTTCTCAG 360
DB 305 GATCAAGAGTGAAGATGGCAATCTCTCTAACAAGATTTATTTGGAGGGTTTCTCAG 364
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTACACAGCAGAACTGCGAGTGTCACT 420
DB 365 GGAGGAGCTTTATCTTTATATCTGCTTACACAGCAGAACTGCGAGTGTCACT 424
QY 421 GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGTCT 480
DB 425 GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGTCT 484
QY 481 AATAGAGATATTCTATTCTCCAGTCCACAGGGATTTGACCCCTTTGGTTCCCTGTATG 540
DB 485 AATAGAGATATTCTATTCTCCAGTCCACAGGGATTTGACCCCTTTAGTTCCCTGTATG 544

QY 541 TTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTTGGTGAATCCAGCCAATGTGACCTTT 600
DB 545 TTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTTGGTGAATCCAGTCAATGTGACCTTT 604
QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCACAGAGAAATATGATGATGTCAGCNA 660
DB 605 AAAACCTATGAAGGTATGATGACAGTTCGTGTCACAGAGAAATATGATGATGTCAGCNA 664
QY 661 TTCATTGATAAATCTCTACCTCCATTCATTTGATGACCTCACTAAGAGGCCTT 710
DB 665 TTCATTGATAAATCTCTACCTCCATTCATTTGATGACCTCACTAAGAGGCCTT 714

RESULT 8
AUI33073

LOCUS
DEFINITION
AUI33073 NT2RP4 Homo sapiens cDNA clone NT2RP4001208 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AUI33073
AUI33073.1 GI:10993612
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
1 (bases 1 to 774)
Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
Isogai,T.
HRI human CDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T.,
Sugano,S., Masuho,Y., Isogai,T.)
Unpublished (2000).

JOURNAL
COMMENT
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source
Location/Qualifiers
1..774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP4001208"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP4"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 97.3%; Score 690.6; DB 1; Length 774;
Best Local Similarity 99.2%; Pred. No. 7.8e-198;
Matches 704; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 ATGTGGGCAATTAACATGTCACACCCCGCTGCCGCCATCGTCCCGCCCGCGGGAAGGCC 60
DB 36 ATGTGGGCAATTAACATGTCACACCCCGCTGCCGCCATCGTCCCGCCCGCGGGAAGGCC 95
QY 61 ACCGCTCGCGTGAATTTCTGATGATGGAGATGATGCGACGCGATGGCGCAGAGGCC 120
DB 96 ACCGCTCGCGTGAATTTCTGATGATGGAGATGATGCGACGCGATGGCGCAGAGGCC 155
QY 121 TTTCAGAGTATCAGAGTTTCATATCAATATATCTGCCCGATGCGCTGTAGGCCT 180

156	TTTGCAGGTATCAGAAGTTCAATATCAAAATATATCTGCGCGCATGCGCCTCTTTAGGCCT	215
181	GTTACATTTAAATATGAACGTGGCTATGCTTCATGGTTTGATATTAATTGGGCTTTTCAACA	240
216	GTTACATTTAAATATGAACGTGGCTATGCTTCATGGTTTGATATTAATTGGGCTTTTCAACA	275
241	GATTACAGGAGGATGAATCTGGGATTTAAACAGGCAGCAGAAAAATATATAAAGCTTTGATT	300
276	GATTACAGGAGGATGAATCTGGGATTTAAACAGGCAGCAGAAAAATATATAAAGCTTTGATT	335
301	GATCAAGAAGTCAGAAATGGCAATTCCTTCTAACAGAAATATTTTTCGGAGGGTTTTCTCAG	360
336	GATCAAGAAGTCAGAAATGGCAATTCCTTCTAACAGAAATATTTTTCGGAGGGTTTTCTCAG	395
361	GGAGGAGCTTTTATCTTTTATATACTGCCCTTACCACACAGCAGAAAACTGCAGGTGTCACT	420
396	GGAGGAGCTTTTATCTTTTATATACTGCCCTTACCACACAGCAGAAAACTGCAGGTGTCACT	455
421	GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGCT	480
456	GCACCTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGCT	515
481	AATAGAGATATTTCTATTCTCAGTGCACGGGGATTTGTGACCCCTTGGTTCCCTCGATG	540
516	AATAGAGATATTTCTATTCTCAGTGCACGGGGATTTGTGACCCCTTGGTTCCCTCGATG	575
541	TTTGGTTCTCTTACGGTGGAAAAATATAAAACATTTGGTGAATCCAGCCTAAATGTGACCTTT	600
576	TTTGGTTCTCTTACGGTGGAAAAATATAAAACATTTGGTGAATCCAGCCTAAATGTGACCTTT	635
601	AAAACCTATGAAGGTATGATGCAC - AGTTTCGTGTCAACAGGAAATGATGGATGTCAAGCA	659
636	AAAACCTATGAAGGTATGATGCACAAAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCA	695
660	ATTCAATGATAAATCCTTCACTCCAAATGATTGACGTCACTAAGAGGCCT	709
696	ATTCAATGATAAATCCTTCACTCCAAATGATTGACGTCACTAAGAGGCCT	745

[illegible]

FEATURES

RESULT 10
BM465006
LOCUS
DEFINITION

Accession	Length	Source	Library	Date
BM465006	1088 bp	mRNA	linear	EST 05-FEB-2002
AGENCOURT	NIH MGC 85	Homo sapiens	cdna clone	IMAGE5505154

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/clone="IMAGE:5274938"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript K1+; Site 1: BamHI; Site 2: SalI-XhoI
gtcgag); oligo-dt primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH MGC library."

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ORIGIN

	Query Match	95.7%	Score 679.4;	DB 3;	Length 711;			
	Best Local Similarity	99.9%;	Pred. No. 1.9e-194;					
	Mismatches	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	ATGTGGCGCAATAACATGTCAAACCCCGTGC	CGCCCATCTGTCGCCGCGCCCGAAGGCC	60				
Db	31	ATGTGGCGCAATAACATGTCAAACCCCGTGC	CGCCCATCTGTCGCCGCGCCCGAAGGCC	90				
Qy	61	ACCCTCGGGTGATTTTCTGTGATGGAGATCT	TGGGAGATCTGGGCGCAGGATGGSCAGAAGCC	120				
Db	91	ACCCTCGGGTGATTTTCTGTGATGGAGATCT	TGGGAGATCTGGGCGCAGGATGGSCAGAAGCC	150				
Qy	121	TTTTGACGGTATCAGAAGTTCAATATCAAATAT	ATCTGTCGCCGCGATCGCCCTGTTAGGCGT	180				
Db	151	TTTTGACGGTATCAGAAGTTCAATATCAAATAT	ATCTGTCGCCGCGATCGCCCTGTTAGGCGT	210				
Qy	181	GTTACATTAAATATGAACGTGGCTATGCCTTC	ATGGTTTGATATTTATTTGGGCTTTCAACA	240				
Db	211	GTTACATTAAATATGAACGTGGCTATGCCTTC	ATGGTTTGATATTTATTTGGGCTTTCAACA	270				
Qy	241	GATTTACAGGAGGATGAATCTGGGATTAACA	CAGGCAGCAGAAAAATATAAAAAGCTTTGATT	300				
Db	271	GATTTACAGGAGGATGAATCTGGGATTAACA	CAGGCAGCAGAAAAATATAAAAAGCTTTGATT	330				
Qy	301	GATCAAGAAGTGAAGAATGGCAITTCCTTCTA	AACAGAAATATTTTGGGAGGGTTTTCTCAG	360				
Db	331	GATCAAGAAGTGAAGAATGGCAITTCCTTCTA	AACAGAAATATTTTGGGAGGGTTTTCTCAG	390				
Qy	361	GGAGGACTTTATCTCTTATATACATGCCCC	TACACACAGCAGAGAACTGGCAGGTCTCACT	420				
Db	391	GGAGGACTTTATCTCTTATATACATGCCCC	TACACACAGCAGAGAACTGGCAGGTCTCACT	450				
Qy	421	GCATCTCAGTTGCTGGCTTCCAATTTCGGGCT	TTCCCCTTCCAAGGGTCTTATCGTGGTGCT	480				
Db	451	GCATCTCAGTTGCTGGCTTCCAATTTCGGGCT	TTCCCCTTCCAAGGGTCTTATCGTGGTGCT	510				
Qy	481	AATAGAGATATTTCTATCTCCAGTGCCACG	GGGATTTGTGACCTTTGGTTCCCTCTGATG	540				
Db	511	AATAGAGATATTTCTATCTCCAGTGCCACG	GGGATTTGTGACCTTTGGTTCCCTCTGATG	570				
Qy	541	TTTTGGTTCTTTACGGTGGAAAACTAAAAA	CATTGTGTGAATCCAGCACAATGTGACCTTT	600				
Db	571	TTTTGGTTCTTTACGGTGGAAAACTAAAAA	CATTGTGTGAATCCAGCACAATGTGACCTTT	630				
Qy	601	AAAAACCTATGAAGTATGATGCACAGTTTC	GTGTCAACAGGAAATGATGGATGTCAAGCAA	660				
Db	631	AAAAACCTATGAAGTATGATGCACAGTTTC	GTGTCAACAGGAAATGATGGATGTCAAGCAA	690				
Qy	661	TTCAATTGATAAACCTCTACCT	681					
Db	691	TTCAATTGATAAACCTCTACCT	711					

RESULT 10
BM465006
LOCUS
DEFINITION

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5', mRNA sequence.
ACCESSION BM465006
VERSION BM465006.1 GI:18514048
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1088)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12147 row: k column: 11
High quality sequence stop: 563.
Location/Qualifiers
1..1088
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:550154"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
/Note="Organ: lymph; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
Source
1..1088
895 bp mRNA linear EST 18-APR-2001
BG614082
602641734F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772673 5',
mRNA sequence.
BG614082
BG614082.1 GI:13665453
ACCESSION
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1643 row: c column: 10
High quality sequence stop: 668.
Location/Qualifiers
1..895
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4772673"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/Note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctggcc); Site_2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGCGCATTTAGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dt(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 95.0%; Score 674.8; DB 2; Length 895;
Best Local Similarity 98.7%; Pred. No. 5.1e-193;
462 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTTTCCAGGGTCTTATCGGTGCT 521
481 AATAGAGATATTTCTATTCTCCAGTGCCACGGGGATTGTGACCCCTTTGGTTCCCTCGATG 540
522 AATAGAGATATTTCTATTCTCCAGTGCCACGGGGATTGTGACCCCTTTGGTTCCCTCGATG 581
541 TTTGGTCTCTTACGGTGGAAAAAATAAAACATTGGTCAATCCAGCCCAATGACCTTT 600
582 TTTGGTCTCTTACGGTGGAAAAAATAAAACATTGGTCAATCCAGCCCAATGACCTTT 641
601 AAAACCTATGAAGGTATGATGCACAGTTCTGTCTCAACAGGAATGATGATGATCAAGCA 660
642 AAAACCTATGAAGGTATGATGCACAGTTCTGTCTCAACAGGAATGATGATGATGATGATG 700
661 TTCAATTGATAAATCTCTACCTCCAATTGATTGACGCTCACTAAGAGGCTTT 710
701 TTCAATTGATAAATCTCTACCTCCAATTGATTGACGCTCACTAAGAGGCTTT 749

RESULT 11
BG614082
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT
FEATURES
Source
1..895
95.4%; Score 677.6; DB 3; Length 1088;
Query Match 98.9%; Pred. No. 7.6e-194;
Matches 702; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
QY 1 ATGTGGCGCAATACATGTCAACCCGCTGCCCGCATCTGTCGCCGCGCCGCGGAGGCC 60
DB 42 ATGTGGCGCAATACATGTCAACCCGCTGCCCGCATCTGTCGCCGCGCCGCGGAGGCC 101
QY 61 ACCGCTGCGGTGATTTCTCGATGGATTGGGAGATACCTGGGCACGATGGGCAGAGCC 120
DB 102 ACCGCTGCGGTGATTTCTCGATGGATTGGGAGATACCTGGGCACGATGGGCAGAGCC 161
QY 121 TTTCAGAGGTATCAGAAAGTTACATATCAATATATCTGCCGATGCGCTGTAGGCTT 180
DB 162 TTTCAGAGGTATCAGAAAGTTACATATCAATATATCTGCCGATGCGCTGTAGGCTT 221
QY 181 GTTACATTAATATGAAGTGGCTATGCTTCATGTTTATATTTGGCTTTTCCACCA 240
DB 222 GTTACATTAATATGAAGTGGCTATGCTTCATGTTTATATTTGGCTTTTCCACCA 281
QY 241 GATTTCAGAGGATCAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGATT 300
DB 282 GATTTCAGAGGATCAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGATT 341
QY 301 GATCAGAGAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 342 GATCAGAGAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 401
QY 361 GGAGGAGCTTTATCTTTTATATCTGCTTACACAGCAGAACTGCGAGTGTCACT 420
DB 402 GGAGGAGCTTTATCTTTTATATCTGCTTACACAGCAGAACTGCGAGTGTCACT 461
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 480
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Matches 701; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY 1 ATGTGGCGCAATAAATGATGCAACCGCGTCCCGCGCATCGTCCCGCGCGCGCGGAGGCC 60
Db 40 ATGTGGCGCAATAAATGATGCAACCGCGTCCCGCGCATCGTCCCGCGCGCGGAGGCC 99
QY 61 ACCGCTGCGGCGTATTTCTGTCATGATGATGGAGATATCGGCGACGATGGCGAGAGCC 120
Db 100 ACCGCTGCGGCGTATTTCTGTCATGATGATGGAGATATCGGCGACGATGGCGAGAGCC 159
QY 121 TTTCAGGATATCAGAAGTTCAATATCAATATATATCGCCCGCATCGCGCTGTAGGCT 180
Db 160 TTTCAGGATATCAGAAGTTCAATATCAATATATATCGCCCGCATCGCGCTGTAGGCT 219
QY 181 GTTACATTAATATGAACGTCGTCATGCTTCAATGTTTGTATATTTGGGCTTTACCA 240
Db 220 GTTACATTAATATGAACGTCGTCATGCTTCAATGTTTGTATATTTGGGCTTTACCA 279
QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGCGACAGAAATATAAAGCTTTGATT 300
Db 280 GATTCACAGGAGATGAATCTGGGATTAACAGGCGACAGAAATATAAAGCTTTGATT 339
QY 301 GATCAAGAGTGAAGATGGCATCTTCTTAACAGAAATATTTTGGAGGTTTCTCAG 360
Db 340 GATCAAGAGTGAAGATGGCATCTTCTTAACAGAAATATTTTGGAGGTTTCTCAG 399
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAAATGCGAGGTGTCAT 420
Db 400 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAAATGCGAGGTGTCAT 459
QY 421 GCACTCAGTGTGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTTATCGGTGCT 480
Db 460 GCACTCAGTGTGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTTATCGGTGCT 519
QY 481 AATAGAGATATTTCTATCTCAGTCCAGCGGATGTCACCTTTGGTCCCTCAGT 540
Db 520 AATAGAGATATTTCTATCTCAGTCCAGCGGATGTCACCTTTGGTCCCTCAGT 579
QY 541 TTGTGTTCTTACGCGTGAAGAACTAAAAAATTCGTGAATCCAGCAATGTGACCTTT 600
Db 580 TTGTGTTCTTACGCGTGAAGAACTAAAAAATTCGTGAATCCAGCAATGTGACCTTT 639
QY 601 AAAACCTATGAAGTATGATGACAGTTCGTGTCACAGGAAATGATGATGTCAGCAA 660
Db 640 AAAACCTATGAAGTATGATGACAGTTCGTGTCACAGGAAATGATGATGTCAGCAA 698
QY 661 TTCAATTGATAA-ACTCCTACCTCCAATGATGATGATGATGATGATGATGATGATGAT 709
Db 699 TTCAATGATAAAGACTCCTACCTCCAATGATGATGATGATGATGATGATGATGATGAT 748
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RESULT 12
BQ227373
LOCUS BQ227373
DEFINITION AGENCOURT_7566147 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6043585
5' mRNA sequence.
ACCESSION BQ227373
VERSION BQ227373.1 GI:20408773
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13284 row: n column: 02
High quality sequence stop: 560.

FEATURES

source
1..889
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="IMAGE:6043585"
/clone="IMAGE:6043585"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.8%; Score 673.2; DB 3; Length 889;
Best Local Similarity 98.5%; Pred. No. 1.6e-192;
Matches 700; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 1 ATGTGGCGCAATAAATGATGCAACCGCGTCCCGCGCATCGTCCCGCGCGCGGAGGCC 60
Db 4 ATGTGGCGCAATAAATGATGCAACCGCGTCCCGCGCATCGTCCCGCGCGCGGAGGCC 63
QY 61 ACCGCTGCGGCGTATTTCTGTCATGATGATGGAGATATCGGCGACGATGGCGAGAGCC 120
Db 64 ACCGCTGCGGCGTATTTCTGTCATGATGATGGAGATATCGGCGACGATGGCGAGAGCC 122
QY 121 TTTCAGGATATCAGAAGTTCAATATCAATATATCTGCCCGCATGCGCTGTAGGCT 180
Db 123 TTTCAGGATATCAGAAGTTCAATATCAATATATCTGCCCGCATGCGCTGTAGGCT 182
QY 181 GTTACATTAATATGAACGTCGTCATGCTTCAATGTTTGTATATTTGGGCTTTACCA 240
Db 183 GTTACATTAATATGAACGTCGTCATGCTTCAATGTTTGTATATTTGGGCTTTACCA 242
QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGCGACAGAAATATAAAGCTTTGATT 300
Db 243 GATTCACAGGAGATGAATCTGGGATTAACAGGCGACAGAAATATAAAGCTTTGATT 302
QY 301 GATCAAGAGTGAAGATGCGCATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 360
Db 303 GATCAAGAGTGAAGATGCGCATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 362
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACCAACAGCAGAAATGCGAGGTGTCAC 420
Db 363 GGAGGAGCTTTATCTTTATATATCTGCTTACCAACAGCAGAAATGCGAGGTGTCAC 422
QY 421 GCACTCAGTGTGCTTCCACTTCCGCGCTTCCCTTCCACAGGTCCTATCGGTGCT 480
Db 423 GCACTCAGTGTGCTTCCACTTCCGCGCTTCCCTTCCACAGGTCCTATCGGTGCT 482
QY 481 AATAGAGATATTTCTATCTCAGTCCAGCGGATGTCACCTTTGGTTCCTCCTGATG 540
Db 483 AATAGAGATATTTCTATCTCAGTCCAGCGGATGTCACCTTTGGTTCCTCCTGATG 542
QY 541 TTGTGTTCTTACGCGTGAAGAACTAAAAAATTCGTGAATCCAGCAATGTGACCTTT 600
Db 543 TTGTGTTCTTACGCGTGAAGAACTAAAAAATTCGTGAATCCAGCAATGTGACCTTT 602
QY 601 AAAACCTATGAAGTATGATGACAGTTCGTGTCACAGGAAATGATGATGTCAGCAA 660
Db 603 AAAACCTATGAAGTATGATGACAGTTCGTGTCACAGGAAATGATGATGTCAGCAA 662
QY 661 TTCAATTGATAA-ACTCCTACCTCCA-ATTGATGACGCTCACTAAGAGGCTT 710
Db 663 TTCAATTGATAA-ACTCCTACCTCCA-ATTGATGACGCTCACTAAGAGGCTT 713

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RESULT 13
BI906551
LOCUS      691 bp      mRNA      linear      EST 16-OCT-2001
DEFINITION 603064126F1 NTH_MGC_118 Homo sapiens cDNA clone IMAGE:5213143 5',
            mRNA sequence.
ACCESSION  BI906551
VERSION    BI906551.1 GI:16169292
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE  1 (bases 1 to 691)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1535 row: d column: 08
            High quality sequence stop: 689.
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                /clone="IMAGE:5213143"
                /tissue_type="Leukocyte"
                /lab_host="DH10B"
                /clone_lib="NIH_MGC_118"
                /note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                (destroyed); RNA source leukocytes from anonymous pool of
                non-activated adult donors. Library is oligo-dr primed
                and directionally cloned (EcoRV site is destroyed upon
                cloning). Average insert size 1.7 kb, insert size range
                1.2-3.3 kb. Library is normalized and enriched for
                full-length clones and was constructed by C. Gruber
                (Invitrogen). Research Genetics tracking code 027. Note:
                this is a NIH_MGC Library."

ORIGIN
Query Match      94.4%; Score 670.4; DB 3; Length 691;
Best Local Similarity 99.7%; Pred. No. 1e-191;
Matches 682; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1  ATGTGGCGCAATAACATGTCAACCCCGTGGCCGATCGTCCCGCCGCGCCGCGAAGGCC 60
Db      9  ATGTGGCGCAATAACATGTCAACCCCGTGGCCGATCGTCCCGCCGCGCCGCGAAGGCC 67

QY      61  ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 120
Db      68  ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 127

QY      121  TTTCAGGATTCAGAGTTTCAATATATATCTGCGCCGATGCGCTGTAGGCCT 180
Db      128  TTTCAGGATTCAGAGTTTCAATATATCTGCGCCGATGCGCTGTAGGCCT 187

QY      181  GTTACATTAATAATGAACGTGGTATCGCTTCATGTTTGGATTAATTTGGCTTTTCAACCA 240
Db      188  GTTACATTAATAATGAACGTGGTATCGCTTCATGTTTGGATTAATTTGGCTTTTCAACCA 247

QY      241  GATTTCACGAGGATCAATCTGGGATTAACAGGCAGCAGAAATAATAAAGCTTTGATT 300
Db      248  GATTTCACGAGGATCAATCTGGGATTAACAGGCAGCAGAAATAATAAAGCTTTGATT 307
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QY      301  GATCAAGAAGTGAGAATGGCATTCCTTCTAAACAGAAATATTTGGGAGGGTTTCTCAG 360
Db      308  GATCAAGAAGTGAGAATGGCATTCCTTCTAAACAGAAATATTTGGGAGGGTTTCTCAG 367

QY      361  GGAGAGCTTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGCAGGTGTCACT 420
Db      368  GGAGAGCTTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGCAGGTGTCACT 427

QY      421  GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGCT 480
Db      428  GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGCT 487

QY      481  AATAGAGATATTTCTATTTCTCCAGTGCACACGGGGATTTGACCCCTTTGGTTCCCTTGATG 540
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QY      541  TTTGTTCTCTTACCGTGGAAAAAATAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 600
Db      548  TTTGTTCTCTTACCGTGGAAAAAATAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 607

QY      601  AAAACCTATGAGGTATGATGCACAGTTCGTCTCAACAGGAAATGATGATGTCAAGCAA 660
Db      608  AAAACCTATGAGGTATGATGCACAGTTCGTCTCAACAGGAAATGATGATGTCAAGCAA 667

QY      661  TTCAATTGATAAACTCCTACCTCCA 684
Db      668  TTCAATTGATAAACTCCTACCTCCA 691

RESULT 14
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LOCUS      796 bp      mRNA      linear      EST 01-AUG-2002
DEFINITION AUI32495 NT2RP3 Homo sapiens cDNA clone NT2RP3004603 5', mRNA
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ACCESSION  AUI32495
VERSION    AUI32495.1 GI:10992849
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE  1 (bases 1 to 796)
AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
            HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
            Location/Qualifiers
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                /clone_lib="NT2RP3"
                /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
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Query Match 93.2%; Score 661.4; DB 1; Length 796;
Best Local Similarity 97.9%; Pred. No. 5.8e-189;
Matches 699; Conservative 0; Mismatches 11; Indels 4; Gaps 3;

QY 1 ATGTGGCGGCAATACATGTCACACCGCGCTGCGCGCCATCGTGCCTGCGCGCGCGGAGGCC 60
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QY 61 ACCGCTGCGCGTGAATTTCTCGCATGATTTGGGAGATCTGGGACGATGGGCGAGAGCC 120
DB 139 ACCGCTGCGCGTGAATTTCTCGCATGATTTGGGAGATCTGGGACGATGGGCGAGAGCC 198

QY 121 TTTCAGGATATCAGAGTTTCAATATCAATATATCTGCGCGATCGGCTGTAGGCTT 180
DB 199 TTTCAGGATATCAGAGTTTCAATATCAATATATCTGCGCGATCGGCTGTAGGCTT 258

QY 181 GTTACATTAATATGATGAACGCGGTATGCGCTTCAATGTTTGAATATTTGGCTTTCACCA 240
DB 259 GTTACATTAATATGATGAACGCGGTATGCGCTTCAATGTTTGAATATTTGGCTTTCACCA 318

QY 241 GATTCACAGGATCAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT 300
DB 319 GATTCACAGGATCAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT 378

QY 301 GATCAAGAGTGAAGATGCAATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 360
DB 379 GATCAAGAGTGAAGATGCAATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 438

QY 361 GGAGGAGCTTATCTTTATATATCTGCGCTTACACACAGCAGAACTGGCAGGTGTCAC 420
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QY 421 GCACCTAGTGTGCGCTTCCACATCTGGGCTTCCCTTCCACAGGCTCTATCGGTGTGCT 480
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QY 541 TTTCAGGATATTTCTATTTCTCCAGTCCACGCGGATTTGACCTTTGGTTCCTCCGTGATG 600
DB 619 TTTCAGGATATTTCTATTTCTNCAGTCCACGCGGATTTGACCTTTGGTTCCTCCGTGATG 678

QY 601 ARAACCTATGAAGTATGATGCAC-AGTTTCGTCAAC-AGGAAATGATGATGTCAGC 658
DB 679 ARAACCTATGAAGTATGATGCACAGTGTGTCACAGGAAATGATGATGTCAGC 738

QY 659 AATTCATTGATAAATCTCTACC--TCCAAATGATTGACGTCACCTAAGAGCCCTT 710
DB 739 AATTCATTGATAAATCTCTACCCTCCAAATGATTGATGAGTCACTTAAAGGCCCTT 792

RESULT 15
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LOCUS 602579913F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4719051 5',
DEFINITION mRNA sequence.
ACCESSION BG528464
VERSION BG528464.1 GI:13520001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 896)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-x@mail.nih.gov
Tissue Procurement: DCTD/DTF
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cdna Library Preparation: CLONETECH Laboratories, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1571 row: i column: 04
High quality sequence stop: 697.
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI
(ggcatattggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.5
kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 93.0%; Score 660.4; DB 2; Length 896;
Best Local Similarity 97.5%; Pred. No. 1.2e-188;
Matches 692; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

QY 1 ATGTGGCGGCAATACATGTCACACCGCGCTGCGCGCCATCGTGCCTGCGCGCGCGGAGGCC 60
DB 17 ATGTGGCGGCAATACATGTCACACCGCGCTGCGCGCCATCGTGCCTGCGCGCGCGGAGGCC 76

QY 61 ACCGCTGCGCGTGAATTTCTCGCATGATTTGGGAGATCTGGGACGATGGGCGAGAGCC 120
DB 77 ACCGCTGCGCGTGAATTTCTCGCATGATTTGGGAGATCTGGGACGATGGGCGAGAGCC 136

QY 121 TTTCAGGATATCAGAGTTTCAATATCAATATATCTGCGCGATCGGCTGTAGGCTT 180
DB 137 TTTCAGGATATCAGAGTTTCAATATCAATATATCTGCGCGATCGGCTGTAGGCTT 196

QY 181 GTTACATTAATATGAACGCGCTATGCTTCAATGTTTGAATATTTGGGCTTTCACCA 240
DB 197 GTTACATTAATATGAACGCGCTATGCTTCAATGTTTGAATATTTGGGCTTTCACCA 256

QY 241 GATTCACAGGATGCAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT 300
DB 257 GATTCACAGGATGCAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT 316

QY 301 GATCAAGAGTGAAGATGCAATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 360
DB 317 GATCAAGAGTGAAGATGCAATCTCTTCAACAGAAATATCTCGGAGGTTTCTCAG 376

QY 361 GGAGGAGCTTATCTTTATATATCTGCGCTTACACACAGCAGAACTGGCAGGTGTCAC 420
DB 377 GGAGGAGCTTATCTTTATATATCTGCGCTTACACACAGCAGAACTGGCAGGTGTCAC 436

QY 421 GCACCTAGTGTGCGCTTCCACATCTCGGCTTCCCTTCCACAGGCTCTATCGGTGTGCT 480
DB 437 GCACCTAGTGTGCGCTTCCACATCTCGGCTTCCCTTCCACAGGCTCTATCGGTGTGCT 496

QY 481 AATAGAGATATTTCTATTTCTCCAGTCCACGCGGATTTGACCTTTGGTTCCTCCGTGATG 540
DB 497 AATAGAGATATTTCTATTTCTCCAGTCCACGCGGATTTGACCTTTGGTTCCTCCGTGATG 556

QY 541 TTTCAGGATATTTCTATTTCTCCAGTCCACGCGGATTTGACCTTTGGTTCCTCCGTGATG 600
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cdna Library Preparation: CLONETECH Laboratories, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1571 row: i column: 04
High quality sequence stop: 697.
Location/Qualifiers
1..896
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4719051"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI
(ggcatattggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.5
kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES
source

557	-TTGGTTCCTTACCGTGGAAAAACT-AAAACATTGGTGAATCAGCCCAATGTGACCTTT	614
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601	AAAACCTATGAAGGATGATGCAAGTTCGTCTCAACAGGAAATGATGATGTCACGAA	660
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615	AAAACCTATGAAGGATGATGACACAGTTCGTCTCAACAGGAAATGATGATGTCACGCA	674
Db		
661	TTCATTGATAAACCCTACCTCCAAATTGATTGACGTCACTAAGAGGCCTT	710
Qy		
675	ATTCATTGATAACTCCTAACTCCAAATTGATTGACGTCACTAAGAGGCCTT	724
Db		

Search completed: April 14, 2006, 13:36:50
Job time : 3949 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:39:47 ; Search time 821 Seconds
(without alignments)
7151.350 Million cell updates/sec

Title: US-09-493-601B-1

Perfect score: 710
Sequence: 1 atgtgcggcaatacatgtc.....tgacgtcactaagagccctt 710

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*

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- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
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- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
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- 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	708.4	99.8	1486	7 US-10-236-417-63	Sequence 63, Appl
2	708.4	99.8	1556	9 US-10-756-149-3671	Sequence 3671, Ap
3	708.4	99.8	2417	3 US-09-813-358-221	Sequence 221, App
4	708.4	99.8	2417	3 US-09-997-279-221	Sequence 221, App
5	708.4	99.8	2417	7 US-10-647-426-14	Sequence 14, Appl
6	708.4	99.8	2493	3 US-09-925-299-218	Sequence 218, App
7	708.4	99.8	2493	3 US-09-925-299-218	Sequence 218, App
8	708.4	99.8	2600	8 US-10-357-930-25196	Sequence 25196, A
9	686.4	96.7	1538	9 US-10-450-763-7268	Sequence 7268, Ap
10	668.4	94.1	701	7 US-10-210-130-55	Sequence 55, Appl
11	668.4	94.1	701	7 US-10-236-417-59	Sequence 59, Appl
12	604.4	85.1	2417	5 US-10-237-271-19	Sequence 19, Appl
13	566.4	79.8	2408	6 US-10-131-487A-156	Sequence 156, App
14	565	79.6	2396	5 US-10-106-698-1516	Sequence 1516, Ap
15	552.8	77.9	709	3 US-09-988-982-2	Sequence 2, Appli
16	495.2	69.7	521	8 US-10-696-639-1549	Sequence 1549, Ap
17	489.8	69.0	624	4 US-09-925-065A-624562	Sequence 624562,
18	489.8	69.0	624	4 US-09-925-065A-624563	Sequence 624563,
19	489.8	69.0	624	4 US-09-925-065A-624564	Sequence 624564,
20	488.2	68.8	624	4 US-09-925-065A-624561	Sequence 624561,
21	408.8	57.6	616	7 US-10-236-417-61	Sequence 61, Appl
22	404.4	57.0	416	3 US-09-878-178-1369	Sequence 1369, Ap
23	404.4	57.0	416	5 US-10-046-935-1369	Sequence 1369, Ap

C	24	404.4	57.0	416	5	US-10-146-502-1369	Sequence 1369, Ap
	25	397.4	56.0	470	8	US-10-696-639-1411	Sequence 1411, Ap
	26	343.4	48.4	441	3	US-09-960-352-3924	Sequence 3924, Ap
	27	277.6	39.1	1624	6	US-10-359-499-15	Sequence 15, Appl
	28	277.6	39.1	1648	9	US-10-956-157-1750	Sequence 1750, Ap
	29	175.8	24.8	3673778	6	US-10-312-841-2	Sequence 2, Appli
	30	172.4	24.3	559	6	US-10-359-499-49	Sequence 49, Appl
	31	157.2	22.1	363	9	US-10-779-543-9796	Sequence 9796, Ap
	32	146.6	20.6	270	9	US-10-450-763-7267	Sequence 7267, Ap
	33	139.4	19.6	423	3	US-09-918-995-34606	Sequence 34606, A
	34	136.6	19.2	1208	10	US-11-097-143-28814	Sequence 28814, A
	35	135	19.0	782	3	US-09-813-358-220	Sequence 220, App
	36	135	19.0	782	3	US-09-997-279-220	Sequence 220, App
	37	128.8	18.1	461	3	US-09-813-358-207	Sequence 207, App
	38	128.8	18.1	461	3	US-09-997-279-207	Sequence 207, App
	39	123.6	17.4	3673778	6	US-10-312-841-1	Sequence 1, Appli
	40	104.4	14.7	106	3	US-09-998-598-2083	Sequence 2083, Ap
	41	100.2	14.1	3917	10	US-11-097-143-28813	Sequence 28813, A
	42	78.6	11.1	105	3	US-09-796-692-5977	Sequence 5977, Ap
	43	78.6	11.1	105	5	US-10-040-862-5977	Sequence 5977, Ap
	44	78.6	11.1	105	6	US-10-057-475B-5977	Sequence 5977, Ap
	45	78.6	11.1	105	6	US-10-154-884B-5977	Sequence 5977, Ap

ALIGNMENTS

RESULT 1
US-10-236-417-63
; Sequence 63, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 63
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(766)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1308)...(1308)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1363)...(1363)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1365)...(1365)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1422)...(1422)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1424)...(1424)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
US-10-236-417-63

Query Match 99.8%; Score 708.4; DB 7; Length 1486;
Best Local Similarity 99.9%; Pred. No. 9.1e-211;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 60
DB 76 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 135

QY 61 ACCGCTGCGGTGATTTCTCGCATGGATTGGGAGATACCTGGGCACGGATGGGCAGAAGCC 120
DB 136 ACCGCTGCGGTGATTTCTGTCATGGATTGGGAGATACCTGGGCACGGATGGGCAGAAGCC 195

QY 121 TTTCAGGATCAGAAAGTTCAATATCAATATATATCTGCCCGCATCGGCTGTTAGGCCT 180
DB 196 TTTCAGGATCAGAAAGTTCAATATCAATATATATCTGCCCGCATCGGCTGTTAGGCCT 255

QY 181 GTTACATTAATATGAACGTGCTATGCCCTCATGGTTTGATATATTGGGCTTTCAACA 240
DB 256 GTTACATTAATATGAACGTGCTATGCCCTCATGGTTTGATATATTGGGCTTTCAACA 315

QY 241 GATTCACAGGAGGATGAATCTGGGATTAACAGGACGAGAGAAAATATAAAGCTTTGATT 300
DB 316 GATTCACAGGAGGATGAATCTGGGATTAACAGGACGAGAGAAAATATAAAGCTTTGATT 375

QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATATTGTTGGAGGGTTTCTCAG 360
DB 376 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATATTGTTGGAGGGTTTCTCAG 435

QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGAGAACTGGCAGGTGTCACCT 420
DB 436 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGAGAACTGGCAGGTGTCACCT 495

QY 421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGGTCT 480
DB 496 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGGTCT 555

QY 481 AATAGAGATATTTCTATCTCCAGTGCCACGGGGATGTGACCTTTGGTTCCCTCGATG 540
DB 556 AATAGAGATATTTCTATCTCCAGTGCCACGGGGATGTGACCTTTGGTTCCCTCGATG 615

QY 541 TTGTTGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 600
DB 616 TTGTTGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 675

QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 660
DB 676 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 735

QY 661 TTTCATTGATAAACTCCTACCTCCAAATTTGATGTCGTCACCTTAAGAGCCCTT 710
DB 736 TTTCATTGATAAACTCCTACCTCCAAATTTGATGTCGTCACCTTAAGAGCCCTT 785

RESULT 2
US-10-756-149-3671
; Sequence 3671, Application US/10756149
; Publication No. US20050181375A1

; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3671
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-3671

Query Match 99.8%; Score 708.4; DB 9; Length 1556;
Best Local Similarity 99.9%; Pred. No. 9.4e-211;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 60
DB 195 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 254

QY 61 ACCGCTGCGGTGATTTCTCGCATGGATTGGGAGATACCTGGGCACGGATGGGCAGAAGCC 120
DB 255 ACCGCTGCGGTGATTTCTCGCATGGATTGGGAGATACCTGGGCACGGATGGGCAGAAGCC 314

QY 121 TTTCAGGATCAGAAAGTTCAATATCAATATATATCTGCCCGCATCGGCTGTTAGGCCT 180
DB 315 TTTCAGGATCAGAAAGTTCAATATCAATATATATCTGCCCGCATCGGCTGTTAGGCCT 374

QY 181 GTTACATTAATATGAACGTGCTATGCCCTCATGGTTTGATATATTGGGCTTTCAACA 240
DB 375 GTTACATTAATATGAACGTGCTATGCCCTCATGGTTTGATATATTGGGCTTTCAACA 434

QY 241 GATTCACAGGAGGATGAATCTGGGATTAACAGGACGAGAGAAAATATAAAGCTTTGATT 300
DB 435 GATTCACAGGAGGATGAATCTGGGATTAACAGGACGAGAGAAAATATAAAGCTTTGATT 494

QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATATTGTTGGAGGGTTTCTCAG 360
DB 495 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATATTGTTGGAGGGTTTCTCAG 554

QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGAGAACTGGCAGGTGTCACCT 420
DB 555 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGAGAACTGGCAGGTGTCACCT 614

QY 421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGGTCT 480
DB 615 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGGTCT 674

QY 481 AATAGAGATATTTCTATCTCCAGTGCCACGGGGATGTGACCTTTGGTTCCCTCGATG 540
DB 675 AATAGAGATATTTCTATCTCCAGTGCCACGGGGATGTGACCTTTGGTTCCCTCGATG 734

QY 541 TTGTTGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 600
DB 735 TTGTTGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCCAATGTGACCTTT 794

QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 660
DB 795 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 854

QY 661 TTTCATTGATAAACTCCTACCTCCAAATTTGATGTCGTCACCTTAAGAGCCCTT 710
DB 855 TTTCATTGATAAACTCCTACCTCCAAATTTGATGTCGTCACCTTAAGAGCCCTT 904

RESULT 3
US-09-813-358-221
; Sequence 221, Application US/09813358
; Patent No. US20020048759A1

Publication No. US20040110197A1
GENERAL INFORMATION:
APPLICANT: Skinner, Michael K.
APPLICANT: Patton, Jodi L.
TITLE OF INVENTION: A METHOD OF DETERMINING TUMOR CHARACTERISTICS BY
TITLE OF INVENTION: DETERMINING ABNORMAL COPY NUMBER OR EXPRESSION LEVEL OF
TITLE OF INVENTION: LIPID-ASSOCIATED GENES
FILE REFERENCE: PATRICK EAGLEMAN: EMBOL-X 252/124
CURRENT APPLICATION NUMBER: US/10/647,426
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US/09/676,052
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 2417
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2417)
OTHER INFORMATION: The sequence of the cDNA coding for
OTHER INFORMATION: Lysophospholipase I
US-10-647-426-14

Query Match 99.8%; Score 708.4; DB 7; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.2e-210; Indels 0; Gaps 0;
Matches 709; Conservative 0; Mismatches 1;
QY 1 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 60
DB 36 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 95
QY 61 ACCGCTGCGGTGATTTTCTGATGATTTGGAGATACCTGGGACCGGATGGGCGAAGGCC 120
DB 96 ACCGCTGCGGTGATTTTCTGATGATTTGGAGATACCTGGGACCGGATGGGCGAAGGCC 155
QY 121 TTTCAGGATACAGAGTTTCAATATCAATATCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 180
DB 156 TTTCAGGATACAGAGTTTCAATATCAATATCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 215
QY 181 GTTACATTAATATGAACCTGGCTATGCCCTTCATGTTTGAATATTTGGGCTTTTCACCA 240
DB 216 GTTACATTAATATGAACCTGGCTATGCCCTTCATGTTTGAATATTTGGGCTTTTCACCA 275
QY 241 GATTACAGGAGATGAATCTGGGATTAACAGGCGAGAGAAAATATAAAGCTTTGATT 300
DB 276 GATTACAGGAGATGAATCTGGGATTAACAGGCGAGAGAAAATATAAAGCTTTGATT 335
QY 301 GATCAGAGATGAAGAAATGGCATTCCTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 360
DB 336 GATCAGAGATGAAGAAATGGCATTCCTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 395
QY 361 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCAACAGAGAAAATCGGAGGTGTCACT 420
DB 396 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCAACAGAGAAAATCGGAGGTGTCACT 455
QY 421 GCATCAGTTGTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGGTCTTAATCGGTGGTGT 480
DB 456 GCATCAGTTGTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGGTCTTAATCGGTGGTGT 515
QY 481 AATAGAGATTTTCTATTTCTCAGTGCACGGGATTTGACCTTTTGGTCCCTGTATG 540
DB 516 AATAGAGATTTTCTATTTCTCAGTGCACGGGATTTGACCTTTTGGTCCCTGTATG 575
QY 541 TTTCGTTCTCTTACGGTGGAAAACTAAAAAATTTGGTGAATTCACAGCAATGTGACCTTT 600
DB 576 TTTCGTTCTCTTACGGTGGAAAACTAAAAAATTTGGTGAATTCACAGCAATGTGACCTTT 635
QY 601 AAAACCTATGAGGATATGATGACAGTTCTGTGTAACAGGAAATGATGATGTCAAGCAA 660
DB 636 AAAACCTATGAGGATATGATGACAGTTCTGTGTAACAGGAAATGATGATGTCAAGCAA 695

QY 661 TTCATTGATAAACTCTTACCTCAATTTGATTGACGTCACTAAGAGGCTTT 710
DB 696 TTCATTGATAAACTCTTACCTCAATTTGATTGACGTCACTAAGAGGCTTT 745
RESULT 6
US-09-925-299-218
Sequence 218, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 2493
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-299-218

Query Match 99.8%; Score 708.4; DB 3; Length 2493;
Best Local Similarity 99.9%; Pred. No. 1.2e-210; Indels 0; Gaps 0;
Matches 709; Conservative 0; Mismatches 1;
QY 1 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 60
DB 100 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 159
QY 61 ACCGCTGCGGTGATTTTCTGATGATTTGGAGATACCTGGGACCGGATGGGCGAAGGCC 120
DB 160 ACCGCTGCGGTGATTTTCTGATGATTTGGAGATACCTGGGACCGGATGGGCGAAGGCC 219
QY 121 TTTCAGGATACAGAGTTTCAATATCAATATCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 180
DB 220 TTTCAGGATACAGAGTTTCAATATCAATATCTGCCCGCATCGTGCCTGCCCGCCCGCGAAGGCC 279
QY 181 GTTACATTAATATGAACCTGGCTATGCCCTTCATGTTTGAATATTTGGGCTTTTCACCA 240
DB 280 GTTACATTAATATGAACCTGGCTATGCCCTTCATGTTTGAATATTTGGGCTTTTCACCA 339
QY 241 GATTACAGGAGATGAATCTGGGATTAACAGGCGAGAGAAAATATAAAGCTTTGATT 300
DB 340 GATTACAGGAGATGAATCTGGGATTAACAGGCGAGAGAAAATATAAAGCTTTGATT 399
QY 301 GATCAGAGATGAAGAAATGGCATTCCTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 360
DB 400 GATCAGAGATGAAGAAATGGCATTCCTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 459
QY 361 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCAACAGAGAAAATCGGAGGTGTCACT 420
DB 460 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCAACAGAGAAAATCGGAGGTGTCACT 519
QY 421 GCATCAGTTGTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGGTCTTAATCGGTGGTGT 480
DB 520 GCATCAGTTGTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGGTCTTAATCGGTGGTGT 579
QY 481 AATAGAGATTTTCTATTTCTCAGTGCACGGGATTTGACCTTTTGGTCCCTGTATG 540
DB 580 AATAGAGATTTTCTATTTCTCAGTGCACGGGATTTGACCTTTTGGTCCCTGTATG 639
QY 541 TTTCGTTCTCTTACGGTGGAAAACTAAAAAATTTGGTGAATTCACAGCAATGTGACCTTT 600
DB 640 TTTCGTTCTCTTACGGTGGAAAACTAAAAAATTTGGTGAATTCACAGCAATGTGACCTTT 699
QY 601 AAAACCTATGAGGATATGATGACAGTTCTGTGTAACAGGAAATGATGATGTCAAGCAA 660

Db 700 AAAACCTATGAAGGTATGATGACAGTTTCGTGTCAACAGGAATGATGATGATCAAGCAA 759
QY 661 TTCAATTGATAAACTCCTACCTCCAAATTTGATTGACAGTCACTAAGAGGCCTT 710
Db 760 TTCAATTGATAAACTCCTACCTCCAAATTTGATTGACAGTCACTAAGAGGCCTT 809

RESULT 7

US-09-925-299-218
; Sequence 218, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 218
; LENGTH: 2493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-299-218

Query Match 99.8%; Score 708.4; DB 3; Length 2493;
Best Local Similarity 99.9%; Pred. No. 1.2e-210;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGATGCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 60
Db 100 ATGTGCGGCAATAAATGATGCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 159
QY 61 ACCGCTGCGGTGATTTCTGATGATGATGGAGATCTGGGACGAGATGGGAGGCC 120
Db 160 ACCGCTGCGGTGATTTCTGATGATGATGGAGATCTGGGACGAGATGGGAGGCC 219
QY 121 TTTCAGGATACAGAGTTCACATATCAATATATCTGCCCGCATCGGCTGTAGGCCT 180
Db 220 TTTCAGGATACAGAGTTCACATATCAATATATCTGCCCGCATCGGCTGTAGGCCT 279
QY 181 GTTACATTAATATGACGTGCTATGCTTCATGTTGATATTTGATATTTGGCTTTCCACCA 240
Db 280 GTTACATTAATATGACGTGCTATGCTTCATGTTGATATTTGGCTTTCCACCA 339
QY 241 GATTACAGGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300
Db 340 GATTACAGGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 399
QY 301 GATCAAGAGTGAAGATGCGATCTCTTAACAGAAATATTTTGGAGGTTTCTCAG 360
Db 400 GATCAAGAGTGAAGATGCGATCTCTTAACAGAAATATTTTGGAGGTTTCTCAG 459
QY 361 GAGGAGCTTTATCTTTATATCTGCTTACACACAGCAGAGAACTGGCAGGTGTCCT 420
Db 460 GAGGAGCTTTATCTTTATATCTGCTTACACACAGCAGAGAACTGGCAGGTGTCCT 519
QY 421 GCACTCAGTTGCTGGCTTCCACATTCGGGCTTCCCTTCCACAGGCTCTCTATCGGTGCT 480
Db 520 GCACTCAGTTGCTGGCTTCCACATTCGGGCTTCCCTTCCACAGGCTCTCTATCGGTGCT 579
QY 481 AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTTGGTTCCCTGATG 540
Db 580 AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTTGGTTCCCTGATG 639
QY 541 TTTCGTTCTCTTACGTTGGAATACTAATAAATTTGTTGATCCAGCAATGTGACCTTT 600
Db 640 TTTCGTTCTCTTACGTTGGAATACTAATAAATTTGTTGATCCAGCAATGTGACCTTT 699

QY 601 AAAACCTATGAAGGTATGATGACAGTTTCGTGTCAACAGGAATGATGATGATCAAGCAA 660
Db 700 AAAACCTATGAAGGTATGATGACAGTTTCGTGTCAACAGGAATGATGATGATCAAGCAA 759
QY 661 TTCAATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTAAGAGGCCTT 710
Db 760 TTCAATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTAAGAGGCCTT 809

RESULT 8

US-10-357-930-25196
; Sequence 25196, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25196
; LENGTH: 2600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2600
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-25196

Query Match 99.8%; Score 708.4; DB 8; Length 2600;
Best Local Similarity 99.9%; Pred. No. 1.3e-210;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGATGCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 60
Db 163 ATGTGCGGCAATAAATGATGCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 222
QY 61 ACCGCTGCGGTGATTTCTGATGATGATGGAGATCTGGGACGAGATGGGAGGCC 120
Db 223 ACCGCTGCGGTGATTTCTGATGATGATGGAGATCTGGGACGAGATGGGAGGCC 282
QY 121 TTTCAGGATACAGAGTTCACATATCAATATATCTGCCCGCATCGGCTGTAGGCCT 180
Db 283 TTTCAGGATACAGAGTTCACATATCAATATATCTGCCCGCATCGGCTGTAGGCCT 342
QY 181 GTTACATTAATATGACGTGCTATGCCCTTCAATGTTGATATTTGGCTTTCCACCA 240
Db 343 GTTACATTAATATGACGTGCTATGCCCTTCAATGTTGATATTTGGCTTTCCACCA 402
QY 241 GATTACAGGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300
Db 403 GATTACAGGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 462

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QY 301 GATCAAGAGTGAAGAAATGGCAATTCCTCTTAACAGAAATTAATTTGGAGGGTTTTCTCAG 360
Db |||||
463 GATCAAGAGTGAAGAAATGGCAATTCCTCTTAACAGAAATTAATTTGGAGGGTTTTCTCAG 522
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCGCTTACCAACAGCAGAAACTGGCAGGTGTCACT 420
Db |||||
523 GGAGGAGCTTTATCTTTTATATATCTGCGCTTACCAACAGCAGAAACTGGCAGGTGTCACT 582
QY 421 GCACCTAGTTGCTGGCTTCCACTTGGGGTTCCTTCCACAGGTCCTATCGTGGTGTCT 480
Db |||||
583 GCACCTAGTTGCTGGCTTCCACTTGGGGTTCCTTCCACAGGTCCTATCGTGGTGTCT 642
QY 481 AATAGAGATTAATTTCTATTTCTCCAGTGCACAGGGGATTTGACCTTTTGGTTCCCTCGATG 540
Db |||||
643 AATAGAGATTAATTTCTATTTCTCCAGTGCACAGGGGATTTGACCTTTTGGTTCCCTCGATG 702
QY 541 TTTGGTTCTCTTACCGTGGAAATACTAAAAAATTTGGTGAATCCAGCCAAATGTGACCTTTT 600
Db |||||
703 TTTGGTTCTCTTACCGTGGAAATACTAAAAAATTTGGTGAATCCAGCCAAATGTGACCTTTT 762
QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGGAATGATGGATGTCAAGCAA 660
Db |||||
763 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGGAATGATGGATGTCAAGCAA 822
QY 661 TTTCAATTGATAAACTCTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 710
Db |||||
823 TTTCAATTGATAAACTCTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 872
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RESULT 9

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US-10-450-763-7268
; Sequence 7268, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 7268
; LENGTH: 1538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-763-7268
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Query Match 96.7%; Score 686.4; DB 9; Length 1538;
Best Local Similarity 99.6%; Pred. No. 7.4e-204;
Matches 709; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCGCCATCGTCCCGCCCGCCGGAAGGCC 60
Db |||||
195 ATGTGGGCAATAACATGTCAACCCCGCTGCCGCCATCGTCCCGCCCGCCGGAAGGCC 254
QY 61 ACCGCTGCGGTGATTTTCTCGATGATTTGGGAGATCTGGGACGCGATGGGCGAGAAGCC 120
Db |||||
255 ACCGCTGCGGTGATTTTCTCGATGATTTGGGAGATCTGGGACGCGATGGGCGAGAAGCC 314
QY 121 TTTGCAAGGTATCAGAAGTTTCAATATATCTGCCCGCATCGCGCTGTGTAGGCCT 180
Db |||||
315 TTTGCAAGGTATCAGAAGTTTCAATATATCTGCCCGCATCGCGCTGTGTAGGCCT 374
QY 181 GTTACATTAATATGAACGTGGCTATGCCTTCATGG-TTTGATATTATTGGGCTTTTACC 239
Db |||||
375 GTTACATTAATATGAACGTGGCTATGCCTTCATGGTTTGTATTATTGGGCTTTTACC 434
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QY 240 AGATTACAGGAGGATGAATCTGGGATTAACACGACGAGAAAAATATATAAAAGCTTTGAT 299
Db |||||
435 AGATTACAGGAGGATGAATCTGGGATTAACACGACGAGAAAAATATATAAAAGCTTTGAT 494
QY 300 TGATCAAGAGTGAAGAAATGGCAATTCCTCTTAACAGAAATTAATTTTGGAGGGTTTTCTC 358
Db |||||
495 TGATCAAGAGTGAAGAAATGGCAATTCCTCTTAACAGAAATTAATTTTGGAGGGTTTTCTC 554
QY 359 AGGAGGAGCTTTATCTTTTATATATCTGCCCTTACCACAGCAGAAAACTGGCAGGTGTCA 418
Db |||||
555 AGGAGGAGCTTTATCTTTTATATATCTGCCCTTACCACAGCAGAAAACTGGCAGGTGTCA 614
QY 419 CTGCACTCAGTTGCTGGCTTCCACTTCCAGTGCACAGGGGATTTGACCCCTTTGGTTCCCTCA 538
Db |||||
615 CTGCACTCAGTTGCTGGCTTCCACTTCCAGTGCACAGGGGATTTGACCCCTTTGGTTCCCTCA 674
QY 479 CTAATAGAGATATTTCTATTCTCCAGTGCACAGGGGATTTGACCCCTTTGGTTCCCTCA 538
Db |||||
675 CTAATAGAGATATTTCTATTCTCCAGTGCACAGGGGATTTGACCCCTTTGGTTCCCTCA 734
QY 539 TGTTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTTGGTGAATCCAGCAATGTGACCT 598
Db |||||
735 TGTTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTTGGTGAATCCAGCAATGTGACCT 794
QY 599 TTAAAACTTATCAGGTATGATGCACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGC 658
Db |||||
795 TTAAAACTTATCAGGTATGATGCACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGC 854
QY 659 AATTCATTGATAAACTCTTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 710
Db |||||
855 AATTCATTGATAAACTCTTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 906
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RESULT 10

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US-10-210-130-55
; Sequence 55, Application US/10210130
; Publication No. US20040014053A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Patturajan, Meera
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Berghs, Constance
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Smithson, Glennda
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Leite, Mario W.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Anderson, David W.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Ort, Tatiana
; APPLICANT: Ellerman, Karen
; APPLICANT: Rastelli, Luca
; APPLICANT: Agee, Michele L.
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Chant, John S.
; APPLICANT: DiPippo, Vincent A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Gangolli, Esha A.
```


Db 8 ATGTGCGCAATAACATGTCACATCCCGCTGCCCATCGTCCCGCCCCCGGAAGGCC 67
QY 61 ACGCTGCGGTGATTTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 120
Db 68 ACCACTGAGGTGATTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 127
QY 121 TTTGAGGATATCAGAAAGTTTCAATATATATCTGCCCATCGGCTCTGTAGGCT 180
Db 128 TTTGCGGTATCATAGTTTCAATATATATCTGCCCATCGGCTCTGTAGGCT 187
QY 181 GTTACATTAATATGAACGTGGCTATGCTTCAATGTTTGAATATTTGGGCTTTCA 240
Db 188 GTTACATTAATATGAACATAGCTATGCTTCAATGTTTGAATATTTGGGCTTTCA 247
QY 241 GATTACAGGAGATGAATCTGGATTAACAGGACGAGAAATATAAAGCTTTGATT 300
Db 248 GATTACAGGAGATGAATCTGGATTAACAGGACGAGAAATATAAAGCTTTGATT 307
QY 301 GATCAAGAGTGAAGATGGCATCTCTTAACAGAAATATTTGGGAGGTTTCTCAG 360
Db 308 GATCAAGAGTGAAGATGGCATCTCTTAACAGAAATATTTGGGAGGTTTCTCAG 367
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAACTGGCAGGTGTCA 420
Db 368 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAACTGGCAGGTGTCA 427
QY 421 GCACCTGAGTGTGGCTTCCACTTGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 480
Db 428 GCACCTGAGTGTGGCTTCCACTTGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 487
QY 481 AATAGAGATATTTCTATCTCAGTGCACAGGAGTTGACCTTTGGTTCCCTGTAG 540
Db 488 AATAGAGATATTTCTATCTCAGTGCACAGGAGTTGACCTTTGGTTCCCTGTAG 547
QY 541 TTTGGTTCTTTACGCTGAAACCTAAACATTTGGTGAATCCAGCCTATGACCTTT 600
Db 548 TTTGGTTCTTTACGCTGAAACCTAAACATTTGGTGAATCCAGCCTATGACCTTT 607
QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTAACAGGAATGATGATGTAAGCA 660
Db 608 AAAACCTATGAAGGTATGATGACAGTTCGTGTAACAGGAATGATGATGTAAGCA 667
QY 661 TTCAATGATAAACTCCTACCTCAATTTGATTGAC 694
Db 668 TTCAATGATAAACTCCTACCTCAATTTGATTGAC 701

RESULT 12
US-10-237-271-19
; Sequence 19, Application US/10237271
; Publication No. US20030096328A1
; GENERAL INFORMATION:
; APPLICANT: THE BURNHAM INSTITUTE
; APPLICANT: SMITH, Jeffrey W.
; APPLICANT: KRIDEL, Steven J.
; APPLICANT: AXELROD, Fumiko T.
; TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS
; FILE REFERENCE: BURN100-1
; CURRENT APPLICATION NUMBER: US/10/237,271
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 60/317,842
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2417)
; OTHER INFORMATION: n is any nucleotide
US-10-237-271-19

Query Match 85.1%; Score 604.4; DB 5; Length 2417;
Best Local Similarity 86.7%; Pred. No. 5,le-178;
Matches 617; Conservative 0; Mismatches 93; Indels 2; Gaps 1;
QY 1 ATGTGCGCAATAACATGTCACATCCCGCTGCCCATCGTCCCGCCCCCGGAAGGCC 60
Db 36 ATGTGCGCAATAACATGTCACATCCCGCTGCCCATCGTCCCGCCCCCGGAAGGCC 95
QY 61 ACGCTGCGGTGATTTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 120
Db 96 ACGCTGCGGTGATTTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 155
QY 121 TTTGAGGATATCAGAAAGTTTCAATATATATCTGCCCATCGGCTCTGTAGGCT 180
Db 156 TTTGAGGATATCAGAAAGTTTCAATATATATCTGCCCATCGGCTCTGTAGGCT 215
QY 181 GTT--ACATTAATAATGAACGTGGCTATGCTTCAATGTTTGAATATTTGGGCTTTCA 238
Db 216 GTTNANCAATTAATATGAACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 275
QY 239 CAGATTTACAGGAGATGAATCTGGATTAACAGGCAGCAGAAATATAAAGCTTTGA 298
Db 276 CAGATTTACAGGAGATGAATCTGGATTAACAGGCAGCAGAAATANNNNNNNNNN 335
QY 299 TTGATCAAGAAGTGAAGAATGGCATTCCTTCTAACAGAAATATTTTGGAGGGTTTCTC 358
Db 336 NNN 395
QY 359 AGGAGGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGAAACTGGCAGGTGA 418
Db 396 NNGGAGGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGAAACTGGCAGGTGA 455
QY 419 CTGCACTCAGTTGCTGGCTTCCACTTGGGCTTCCCTTCCACAGGCTCTATCGGTGG 478
Db 456 CTGCACTCAGTTGCTGGCTTCCACTTGGGCTTCCCTTCCACAGGCTCTATCGGTGG 515
QY 479 CTAATAGAGATATTTCTATTTCTCAGTGCACGGGATTTGACCTTTGGTTCCCTGA 538
Db 516 CTAATAGAGATATTTCTATTTCTCAGTGCACGGGATTTGACCTTTGGTTCCCTGA 575
QY 539 TGTGTTGTTCTCTTACGCTGGAATAAATAAATTTGGTGAATCCAGCAATGTGACCT 598
Db 576 TGTGTTGTTCTCTTACGCTGGAATAAATAAATTTGGTGAATCCAGCAATGTGACCT 635
QY 599 TTAAAACTATGAAGGTATGATGACAGTTCGTGTAACAGGAAATGATGATGTAAGC 658
Db 636 TTAAAACTATGAAGGTATGATGACAGTTCGTGTAACAGGAAATGATGATGTAAGC 695
QY 659 AATTCATTGATAAACTCCTACCTCCAATTTGATTGACGTCACTAAGAGGCTT 710
Db 696 AATTCATTGATAAACTCCTACCTCCAATTTGATTGACGTCACTAAGAGGCTT 747

RESULT 13
US-10-131-487A-156
; Sequence 156, Application US/10131487A
; Publication No. US20040009478A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
; FILE REFERENCE: ALBRE 11
; CURRENT APPLICATION NUMBER: US/10/131,487A
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/623,791A
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/DE99/00721
; PRIOR FILING DATE: 1999-03-09

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; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 2408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-487A-156

Query Match          79.8%; Score 566.4; DB 6; Length 2408;
Best Local Similarity 90.6%; Pred. No. 4.2e-166;
Matches 643; Conservative 0; Mismatches 1; Indels 66; Gaps 1;

QY 1 ATGTGGGCAATAACATGTCACCCCGCTGCGCCCATCGTGCCTCCCGCCCGCGAAGGCC 60
DB 70 ATGTGGGCAATAACATGTCACCCCGCTGCGCCCATCGTGCCTCCCGCCCGCGAAGGCC 129
QY 61 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATACCTGGGACGCGATGGGCGAGAAGCC 120
DB 130 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATACCTGGG----- 170
QY 121 TTTCAGAGGTATCAGAAAGTTCAATATATATCTGCCCGCATCGCGCTGTGTAGGCCT 180
DB 171 -----GCTGTGTAGGCCT 183
QY 181 GTTACATTAAATATGAACGTGGCTATGCCTTCATGTTTGATATATTTGGGCTTTTCACCA 240
DB 184 GTTACATTAAATATGAACGTGGCTATGCCTTCATGTTTGATATATTTGGGCTTTTCACCA 243
QY 241 GATTACAGAGGATGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTTGATT 300
DB 244 GATTACAGAGGATGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTTGATT 303
QY 301 GATCAAGAAGTGAAGAATGSCATTCTCTTAACAGAAATATTATTGGGAGGTTTCTCAG 360
DB 304 GATCAAGAAGTGAAGAATGSCATTCTCTTAACAGAAATATTATTGGGAGGTTTCTCAG 363
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTACACAGACAGAAACTGGCAGGTGTCACT 420
DB 364 GGAGGAGCTTTATCTTTATATCTGCTTACACAGACAGAAACTGGCAGGTGTCACT 423
QY 421 GCACCTAGTTGCTGGCTTCACCTTCCAGTTCGCGGCTTCCCTTCCACAGGCTCTTATCGGTGTGCT 480
DB 424 GCACCTAGTTGCTGGCTTCACCTTCCAGTTCGCGGCTTCCCTTCCACAGGCTCTTATCGGTGTGCT 483
QY 481 AATAGAGATATTCTATTTCTCCAGTGCACGGGATTTGACCTTTTGGTTCCTCCCTGTATG 540
DB 484 AATAGAGATATTCTATTTCTCCAGTGCACGGGATTTGACCTTTTGGTTCCTCCCTGTATG 543
QY 541 TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 544 TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 603
QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAAGCAA 660
DB 604 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAAGCAA 663
QY 661 TTCAATTGATAAACTCTTACCTCAATTTGATTTGACGTCACCTAAGAGGCTTT 710
DB 664 TTCAATTGATAAACTCTTACCTCAATTTGATTTGACGTCACCTAAGAGGCTTT 713

RESULT 14
US-10-106-698-1516
; Sequence 1516, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
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; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1516
; LENGTH: 2396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1516

Query Match          79.6%; Score 565; DB 5; Length 2396;
Best Local Similarity 90.3%; Pred. No. 1.2e-165;
Matches 641; Conservative 1; Mismatches 2; Indels 66; Gaps 1;

QY 1 ATGTGGGCAATAACATGTCACCCCGCTGCGCCCATCGTGCCTCCCGCCCGCGAAGGCC 60
DB 36 ATGTGGGCAATAACATGTCACCCCGCTGCGCCCATCGTGCCTCCCGCCCGCGAAGGCC 95
QY 61 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATACCTGGGACGCGATGGGCGAGAAGCC 120
DB 96 ACCGCTGCGGTGATTTCTGTCATGATTTGGGAGATACCTGG----- 136
QY 121 TTTCAGAGGTATCAGAAAGTTCAATATATATCTGCCCGCATCGCGCTGTGTAGGCCT 180
DB 137 -----GCTGTGTAGGCCT 149
QY 181 GTTACATTAAATATGAACGTGGCTATGCCTTCATGTTTGATATATTTGGGCTTTTCACCA 240
DB 150 GTTACATTAAATATGAACGTGGCTATGCCTTCATGTTTGATATATTTGGGCTTTTCACCA 209
QY 241 GATTACAGAGGATGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTTGATT 300
DB 210 GATTACAGAGGATGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTTGATT 269
QY 301 GATCAAGAAGTGAAGAATGSCATTCTCTTAACAGAAATATTATTGGGAGGTTTCTCAG 360
DB 270 GATCAAGAAGTGAAGAATGSCATTCTCTTAACAGAAATATTATTGGGAGGTTTCTCAG 329
QY 361 GGAGGAGCTTTATCTTTATATATCTGCGCTTACACAGACAGAAACTGGCAGGTGTCACT 420
DB 330 GGAGGAGCTTTATCTTTATATATCTGCGCTTACACAGACAGAAACTGGCAGGTGTCACT 389
QY 421 GCACCTAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCTTATCGGTGTGCT 480
DB 390 GCACCTAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCTTATCGGTGTGCT 449
QY 481 AATAGAGATATTCTATTTCTCCAGTGCACGGGATTTGACCTTTTGGTTCCTCCCTGTATG 540
DB 450 AATAGAGATATTCTATTTCTCCAGTGCACGGGATTTGACCTTTTGGTTCCTCCCTGTATG 509
QY 541 TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 510 TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 569
QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAAGCAA 660
DB 570 AAAACCTATGAAGGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAAGCAA 629
QY 661 TTCAATTGATAAACTCTTACCTCAATTTGATTTGACGTCACCTAAGAGGCTTT 710
DB 630 TTCAATTGATAAACTCTTACCTCAATTTGATTTGACGTCACCTAAGAGGCTTT 679

RESULT 15
```

US-09-988-982-2
: Sequence 2, Application US/09988982
: Patent No. US20020081699A1
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: Shah, Purvi
: Murry, Lynn E.
: TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/988,982
: FILING DATE: 19-No. US20020081699A1-2001
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/213,394
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0269 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 709 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: KIDNNOT19
: CLONE: 2676650
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-988-982-2
Query Match 77.9%; Score 552.8; DB 3; Length 709;
Best Local Similarity 89.9%; Pred. No. 3.8e-162;
Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;
QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCGCGCGCGGAGGCC 60
DB 75 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCGCGCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTCTCGATGATGGAGATCTGGGCACGATGGGCGAGAGGCC 120
DB 135 ACCGCTGCGGTGATTTCTCGATGATGGAGATCTGGG----- 175
QY 121 TTTCAGGTATCAGAGTTACATATACAAATATCTGCCCGCATGCGCTGTAGGCCT 180
DB 176 -----GCCTGTTAGGCCT 188
QY 181 GTTACATTAATATGAACGTGGCTATGCCCTTCATGGTTTGATATATTGGGCTTTCACCA 240
DB 189 GTTACATTAATATGAACGTGGCTATGCCCTTCATGGTTTGATATATTGGGCTTTCACCA 248
QY 241 GATTACACAGGATCAATCTGGGATTTAAACAGGCGAGCAAGAAATATAAAGCTTTGATT 300
DB 249 GATTACACAGGATCAATCTGGGATTTAAACAGGCGAGCAAGAAATATAAAGCTTTGATT 308
QY 301 GATCAAGAGTGAAGATGGCATTCCTTTCTAACAGAAATATTATTTGGAGGGTTTCTCAG 360
DB 309 GATCAAGAGTGAAGATGGCATTCCTTTCTAACAGAAATATTATTTGGAGGGTTTCTCAG 368

QY 361 GGAGGAGCTTTATCTTTATATACTGCCCTTACCACACAGCAAGAACTGGCAGGTGTCACT 420
DB 369 GGAGGAGCTTTATCTTTATATACTGCCCTTACCACACAGCAAGAACTGGCAGGTGTCACT 428
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGT 480
DB 429 GCACCTCAGTTTCTTCTGCTTCCACTTCGGGNTTCTTTTCCACAGGRCCTATCGGTGGTGT 488
QY 481 AATAGAGATATTTCTATTCTCCAGTCCACGGGGATTGTGACCCCTTTTGGTTCCCTGTATG 540
DB 489 AATAGAGATATTTCTATTCTCCAGTCCACGGGGATTGTGACCCCTTTTGGTTCCCTGTATG 548
QY 541 TTTGGTTTCTTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 600
DB 549 TTTGGTTTCTTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 608
QY 601 AAAACCTATGAAGGTATGATGCACAGTTCTGTGTCAACAGGAATGATGGATGTCAAGCAA 660
DB 609 AAAACCTATGAAGGTATGATGCACAGTTCTGTGTCAACAGGAATGATGGATGTCAAGCAA 668
QY 661 TTCATTGATAAACTCCTACCTCCAATTGATTGACGTCACCTA 701
DB 669 TTCATTGATAAACTCCTACCTCCAATTGATTGACGTCACCTA 709

Search completed: April 14, 2006, 16:02:12
Job time : 824 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	Time				
C 1	489.8	69.0	624	6	US-09-925-065A-624562	Sequence 624562, App1	
	489.8	69.0	624	6	US-09-925-065A-624563	Sequence 624563, App1	
C 2	489.8	69.0	624	6	US-09-925-065A-624564	Sequence 624564, App1	
C 3	488.2	68.8	624	6	US-09-925-065A-624565	Sequence 624565, App1	
C 4	488.2	68.8	624	6	US-09-925-065A-624566	Sequence 624566, App1	
C 5	282.4	39.8	1591	14	US-11-136-527-98	Sequence 98, App1	
C 6	68.4	9.6	70	8	US-10-310-914A-5212	Sequence 5212, App1	
C 7	68.2	9.6	852	8	US-09-978-360A-38	Sequence 38, App1	
C 8	63	8.2	86950	8	US-10-857-780-5	Sequence 5, App1	
C 9	58	8.2	90	8	US-10-310-914A-5211	Sequence 5211, App1	
C 10	55	7.7	684	9	US-10-932-182A-3117	Sequence 3117, App1	
C 11	55	7.7	684	9	US-10-932-182A-3117	Sequence 3117, App1	
C 12	53.4	7.5	468	9	US-10-932-182A-82374	Sequence 82374, App1	
C 13	53.4	7.5	468	9	US-10-932-182A-82374	Sequence 82374, App1	
C 14	37.6	5.3	8098	8	US-10-995-561-355	Sequence 255, App1	
C 15	37.6	5.3	10407	8	US-10-995-561-361	Sequence 261, App1	
C 16	37.6	5.3	16792	8	US-10-995-561-362	Sequence 262, App1	
C 17	37.6	5.3	17232	8	US-10-995-561-360	Sequence 260, App1	
C 18	37.6	5.3	17436	8	US-10-995-561-357	Sequence 257, App1	

Qy	121	TTTGCAGGTTATCAGAAAGTTTCACATATCAAAATATATCTGCCCGCATGCGCCTGTGTAGGCCT	180
Db	403	TTTGGCGGTATCATTAAGTTTCACATATCAAAATATATCTGCCCGCATGCGCCTGTGTAGGCCT	344
Qy	181	GTT - ACATTAAATATGAACGTGGCTATGCCTTTCATGGTTTGATATTAATGGGCTTTTCACC	239
Db	343	GTTAACTTAAATATGAACATAGCTATGCCTTTCATGGTTTGATATTAATGGGCTTTTCACC	284
Qy	240	AGATTACAGGAGGATGAATCTGGGATTTAAACACGCGACGAGAAATATAAAAGCTTTTGAT	299
Db	283	AGATTACAGGAGGATGAATCTGGGATTTAAACACGCGACGACAAATATAAAAGCTTTTGAT	224
Qy	300	TGATCAAGAAGTGAAGAATGGCAATCTCTTAAACAGAAATATTTTGGAGAGGTTTTCCTCA	359
Db	223	TGATCAAGAAGTGAAGAATGGCAATCTCTTAAACAGAAATATTTTGGAGAGGTTTTCCTCA	164
Qy	360	GGGAGGAGCTTTATCTTTTATATACATGCCCTTACCAACAGACAGAAACTGGCAGGTGTAC	419
Db	163	GGGAGGAGCTTTATCTTTTATATACATGCCCTTACCAACAGCACCAGAAACTGGCAGGTGTAC	104
Qy	420	TGCACCTCAGTTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGGTCCTATCGGTGTGC	479
Db	103	TGCACCTCAATGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGGTCCTATCGGTGTGC	44
Qy	480	TAATAGAGATATTTCTATTCTCCAGTGCCACGGGGATTGTGAC	522
Db	43	TAATAGAGATATTTCTATTCTCCAGTGCCACGGGGATTGTGAC	1

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RESULT 2
US-09-925-065A-624563/c
; Sequence 624563, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 624563
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-624563

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Qy	181	GTT - ACATTAAATATGAACGTGGCTATGCCCTTCATGGTTTGATATTATTGGCGCTTTCACC	2339
Db	343	GTTAAACATTAAATATGAACATAGCTATGCCCTTCATGGTTTGATATTATTGGCGCTTTCACC	284
Qy	240	AGATTTCACAGGAGATGAATCTCGGGATTAAACAGGCGAGCAGAAATATATAAAGCTTTGAT	299
Db	283	AGATTTCACAGGAGATGAATCTCGGGATTAAACAGGCGAGCACAATAATATAAAGCTTTGAT	224
Qy	300	TGATCAAGAGTCAAGAAATGGCAATTCCTTCTAAACAGAAATTATTTTGGAGGGGTTTTCTCA	359
Db	223	TGATCAAGAGTCAAGAAATGGCAATTCCTTCTAAACAGAAATTATTTTGGAGGGGTTTTCTCA	164
Qy	360	GGGAGGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAAACTGGCAGGTGTCA	419
Db	163	GGGAGGAGCTTTATCTTTATATATCTGCCCTTACCAACGACCCAGAACTGGCAGGTGTCA	104
Qy	420	TGCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCAACGGGTCTATACGGTGGTGC	479
Db	103	TGCACCTCAATTGCTGGCTTCCACTTTGGGCTTCCCTTCCAACGGGTCTATACGGTGGTGC	44
Qy	480	TAATAGAGATATTTCTATTCTCAGTGCCACGGGGATTGTGAC	522
Db	43	TAATAGAGATATTTCTATTCTCAGTGCCACGGGGATTGTGAC	1

```

RESULT 3
US-09-925-065A-624564/c
; Sequence 624564, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 624564
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-624564

```

Query Match	69.08;	Score 489.8;	DB 6;	Length 624;
Best Local Similarity	97.1%;	Pred No. 1.7e-134;		
Matches 508;	Conservative 1;	Mismatches 13;	Indels 1;	Gaps 1;
Qy	1	ATGTGCGGCAATAACATGTCAACCCCGCTGCGCGCCATCTGTGCGCGCGCCCGCGAAGGCC	60	
Db	523	ATGTGCGGCAATAACATGTCAACCCCGCTGCGCGCCATCTGTGCGCGCGCCCGCGAAGGCC	464	
Qy	61	ACCGCTCGGGTGATTTTTCCTGCAATGCGAGATCTGGGACGATCGGGCAGGATGGGCAGAAAGCC	120	
Db	463	ACCACTGAGGTGATTTTTCCTGCAATGCGAGATCTGGGACGATCTGGGACGATGGGCAGAAAGCC	404	
Qy	121	TTTCCAGGTATCAGAAGTTCACATATCAAAATATATCTGCCGGATCGCCCTGTTAGGCCT	180	
Db	403	TTTCCCGGTATCATAAAGTTCACATCAAAATATATCTGCCCGCATCGCCTGTTAGGCCT	344	
Qy	181	GTT-ACATTAAATATGAACGTGGCTATCGCCTCATGGTTTGATATATATGGGCTTTTCACC	239	

Qy	452	CCCTTCCACAGGCTCTATCGGTGGTGTCTAATAGAGATATTTCTATTCTCCAGTGCACG	511
Db	548	ACTTCCCCACAGCAGCAATGCGAGTGCCAAG--GACCTGGCCATCTCTTCAATGCCACG	604
Qy	512	GGGATTGTGACCCCTTTGGTTCCTCCCTGATGTTTGGTTCTTTACGGTGAAAACTAAAA	571
Db	605	GGGAGTGGACCCCAATGGTACCTGTTCGGTTTGGGGCCCTGACAGCTGAGAGGTCGCGA	664
Qy	572	CATTGGTGAATCCAGCCAATGTGACCTTTTAAAACTATGAGGTATATGATGCACAGTTCTG	631
Db	665	CAGTTGTACACTGCCAGGGTCCAGTTTAAAGACATACCCAGGTGTATGCACAGCTCCT	724
Qy	632	GTCAACAGGAAATGATGGATGTCAAGCAATCAATTGATTAACCTCCTACCTCC	683
Db	725	GTCTCTCAGCAGATGCGAGCTGTAAAGAGAAATTTCTGGAGAACTTCTGCCTCC	776

```

RESULT 6
US-10-310-914A-5212
; Sequence 5212, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5212
; LENGTH: 70
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-5212

Query Match          9.6%; Score 68.4; DB 8; Length 70;
Best Local Similarity 62.9%; Pred. No. 3.8e-10;
Matches 44; Conservative 25; Mismatches 1; Indels 0; Gaps 0;

Qy      310  GTGAAGAATGGCATTCTCTTAACAGAAATTATTTGGGAGGAGTCTTCTCAGGAGGAGCT 369
Db      1    GUGAAGAAGUAGGCAUCCUUCUACAGAAUAUUUGGAGGGUUUUUCUACAGGAGGAGCU 60

Qy      370  TTATCTTTAT 379
Db      61  UUAUCUUUAV 70

```

RESULT 7
US-09-978-360A-38
; Sequence 38, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION: Jean-Baptiste Dumas Milne
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56. US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116

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; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 38
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 229..735
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 229..492
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 6.70
; OTHER INFORMATION: seq VFALSSFLNKASA/VY
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 816..821
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 841..852
US-09-978-360A-38

Query Match          9.6%; Score 68.2; DB 5; Length 852;
Best Local Similarity 47.5%; Pred. No. 1.5e-09;
Matches 252; Conservative 0; Mismatches 263; Indels 16; Gaps 1

QY 18  GTCAACCCCGCTGCCCGCCATCGTGGCCGCGCCGGAAGGCCACCGCTGGCGTGATTTT 77
DB 41  GTCGGTTCTGCGAGCGCTGTATCGTGTCCGCGCAGGAGGCGATAGCGGCTCTCTGATCTT 100
QY 78  CCTGCATPGGATGGGAGATACTGGGACGGATGGGCGAAGCCCTT----- 122
DB 101  CCTGCATGGCTCAGGTGATCTGGACAAGGATTAAGAAATGCGATCAAGCAGGTTTTTAA 160
QY 123  -TGCAGGTATCAGNAAGTTCACATATCAATATATCTGCCGCATGCGCTGTAGGCGCTG 181
DB 161  ATCAAGAATTAAACATTCCAACACATAAAATTTATTCCAACAGCTCCTCCAGATCAT 220
QY 182  TTACATTAAATATGAACGTGGCTATGCTTCATGTTTGATATTATTCGGCTTTTACCAG 241
DB 221  ATACTCTTATGAAGAGGAGTAATCTCCAAATGTATGGTTGACAGATTTAAATAACCAATG 280
QY 242  ATTCACAGGAGGATGAATCTGGGATTAAACAGGCGACAGAAAAATATAAAGCTTTGATG 301
DB 281  ACTGCCCAGAACACCTTTGAATCAATTGATGTGATGTGCAAGTGCTTACTGATTTGATG 340
QY 302  ATCAAGAAGTGAAGAAATGGCAATTCCTTCTAAACAGAAATTTTGGGAGGTTTTTCTCAG 361
DB 341  ATGAAGAAGTAAAAAGTGGCATCAAGAAGAAACAGGATATTAAATAGGAGGATTTCTCTAT 400
QY 362  GAGGAGCTTTATCTTTATATACTGCCCTTACACACAGCAGAAACTGGCAGGTGTCACTG 421
DB 401  GAGGATGCATGGCAATGCATTTAGCATATAGAAATCATCAAGATGTGCGCAGAGTATTTG 460
QY 422  CACTCAGTGTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGCTA 481
DB 461  CTCCTTCTAGTTTTCTGAATAAAGCATCTGCTGTTTACCGGCTCTTCAGAAAGAGTAATG 520
QY 482  ATAGAGATATTTCTATTCTTCAGTGCACGGGGATTGTGACCTTTGGTTC 532

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Db 521 GTGACTTCCTGAATTATTTAGTGTGTCATGCTGACTGTCAGATGAGTTAGTTC 571

RESULT 8
US-10-857-780-5
; Sequence 5, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, RICHARD B.
; APPLICANT: KAMMERER, STEPHAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 86950
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2028)..(20282)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (39985)..(39985)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51936)..(51996)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (64732)..(64732)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (83916)..(83919)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (86196)..(86196)
; OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-5
Query Match 8.9%; Score 63; DB 8; Length 86950;
Best Local Similarity 61.1%; Pred. No. 5.1e-07;
Matches 102; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 474 TGTGTCTAATAGATATTTCTATCTCCAGTGCACCGGGGATGTGACCCCTTTGGTTCC 533
Db 54400 TGGCAGTGCACGAGACCTGGCCATCTCCAGTGCACGGAGCTGACCCCATGTGTC 54459
QY 534 CTGTGATGTTGGTTCTTACGGTGGAAAAA CTAATAAAACATTTGGTGAATTCAGCCATGT 593
Db 54460 CGTACGGTTTGGGGCCCTGACGGCTGAGAAGCTCCGGTCTGTTGTGCACACCTGCCAGGT 54519

QY 594 GACCTTTAAACCTATGAAGGTATGATGCACAGTTCTGTCTCAACAGG 640
Db 54520 CCAGTTCAAGACATACCCGGGTGTGATGCACAGCTCCTGTCTCAGG 54566

RESULT 9
US-10-310-914A-5211
; Sequence 5211, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5211
; LENGTH: 90
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-5211
Query Match 8.2%; Score 58; DB 8; Length 90;
Best Local Similarity 86.2%; Pred. No. 5.1e-07;
Matches 50; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATAACATGTCAACCGCTGCCCGCATGCTGCCCGCCCGCGAAGG 58
Db 33 AUGUGCGCAUAUACAUGUCAACCCCGUGCGCCGCAUGCGUGCGCCCGCGAAGG 90

RESULT 10
US-10-932-182A-3117
; Sequence 3117, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3117
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3117
Query Match 7.7%; Score 55; DB 9; Length 684;
Best Local Similarity 46.4%; Pred. No. 1.1e-05;
Matches 252; Conservative 0; Mismatches 285; Indels 6; Gaps 2;

QY 142 CATATCAATATATCTGCCCGCATGCGCTGTAGCCCTGTACATTAAATATGAACGTG 201
Db 139 CACACAAACTTTGTATTCCTCCCAATGCTCCAGAGGTCCATGTGACAGCAACCGTGTGCA 198
QY 202 GCTATGCCCTTCATGTTTGATATTATG---GGCTTTCACAGATTTCACAGAGGATGAA 258
Db 199 TTGATGCCCTGCTTGGTTTGACATCTAGAGTGGGATTTAGTTTTCCTCAAGTTGATAGC 258
QY 259 TCTGGGATTAAACAGCAGCAGCAAAAATATAAAAGCTTTTGATTGATCAAGAAGTGAAGAAT 318
Db 259 GATGATTATCAATTCCTTAATGCCATTTGAAGACCGTTAAACAGGAATTGACAAG 318
QY 319 GGCATTCTCTTAACAGAAATTTATTTGGGAGGTTTTCTCAGGGAGGAGCTTATCTTTA 378

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Db 319 GGCATTAAACCGGAACAGATCATCATTTGGGGGTTCTCTCAAGGTGCTGCATTGGCCCTG 378
QY 379 TATACAGCCCTTACACACAGAGAACTGGCAGGTGTCACTGCACCTAGTTGCTGGCTT 438
Db 379 GCATCATCTGTCACTTTACCATGSAAGTGCAGGTATAGTCGCACATCGGGTTTGGT 438
QY 439 CCACCTTCGGGCTTCCTCCACAGGTCCTATCGGTGGTGTAAATAGAGATATTTCTATT 498
Db 439 TACATTCCGGGAATCTTGAACA---ACACAAGACGATCTCAAGTCAAGACACCCATT 495
QY 499 CTCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATGTTGGTTCTCTTAAGGTG 558
Db 496 TTTACGGACATGGCGATATGATCCAGTTGTACCTATAGCACTTGGCTTGAGCGCAAAA 555
QY 559 GAAAACTTAAACAATTTGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATG 618
Db 556 AAATTTCTACCAAGACCTTGAACA---ACACAAGACGATCTCAAGTCAAGACACCCATT 495
QY 499 CTCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATGTTGGTTCTCTTAAGGTG 558
Db 496 TTTACGGACATGGCGATATGATCCAGTTGTACCTATAGCACTTGGCTTGAGCGCAAAA 555
QY 559 GAAAACTTAAACAATTTGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATG 618
Db 556 AAATTTCTACCAAGACCTTGAACA---ACACAAGACGATCTCAAGTCAAGACACCCATT 495
QY 619 ATGCACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAATTCATTGATAACTCTTA 678
Db 616 GCACATTTACAGTTCTCGAGGAATCGAGCACTTAACTGCCTTCTTTAAGAAATGCCTA 675
QY 679 CCT 681
Db 676 TCT 678
```

```
RESULT 11
US-10-932-182A-3117
; Sequence 3117, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3117
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3117
```

```
Query Match 7.7%; Score 55; DB 9; Length 684;
Best Local Similarity 46.4%; Pred. No. 1.1e-05;
Matches 252; Conservative 0; Mismatches 285; Indels 6; Gaps 2;

QY 142 CATATCAATATATCTGCCGCATCGCCTGTTAGGCTGTTCACATTAATATGAACGTG 201
Db 139 CACAAACTTTGTATTTCCCAATGCTCCAGAGTCCATGTACAGCAAAACGGTGTGCA 198
QY 202 GCTATGCCCTTCATGGTTTGATATTATG---GGCTTTCCACAGATTCACAGGAGGATGAA 258
Db 199 TTGATGCCCTGCTTGGTTTGACATCTAGAGTGGATTCAGTTTTCACAAAGTTGATAGC 258
QY 259 TCTGGATTAAACAGCAGCAAGAAATATAAAGCTTTGATTTGATTCACAGATTCACAGGAGGATGAA 318
Db 259 GATGGATTCATGAATTCCTTAAATGCCATTGAAAAGACGGTTTAAACAGGAAATTGACAAG 318
QY 319 GGCATTTCTTCTAAACAGAAATATTTTGGAGGGTTTCTCAGGAGGAGCTTTATCTTTA 378
Db 319 GGCATTTAAACCGGAACAGATCATCATTTGGGGGTTCTCTCAAGGTGCTGCATTGGCCCTG 378
QY 379 TATACAGCCCTTACACACAGAGAACTGGCAGGTGTCACTGCACCTAGTTGCTGGCTT 438
Db 379 GCATCATCTGTCACTTTACCATGSAAGTGCAGGTATAGTCGCACATCGGGTTTGGT 438
```

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QY 439 CCACCTTCGGGCTTCCTTCACAGGTCCTATCGGTGGTGTAAATAGAGATATTTCTATT 498
Db 439 TACATTCGGGAATCTTGAACA---ACACAAGACGATCTCAAGTCAAGACACCCATT 495
QY 499 CTCAGTGCACGGGATTTGACCCCTTTGGTTCCTCCCTGATGTTGGTTCTCTTAAGGTG 558
Db 496 TTTACGGACATGGCGATATGATCCAGTTGTACCTATAGCACTTGGCTTGAGCGCAAAA 555
QY 559 GAAAACTTAAACAATTTGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATG 618
Db 556 AAATTTCTACCAAGACACCTGCGGGTACAGGATTAAGATTTAAGATTTATAGTGGTATG 615
QY 619 ATGCACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAATTCATTGATAACTCTTA 678
Db 616 GCACATTTACAGTTCTCGAGGAATCGAGCACTTAACTGCCTTCTTTAAGAAATGCCTA 675
QY 679 CCT 681
Db 676 TCT 678
```

```
RESULT 12
US-10-932-182A-82374
; Sequence 82374, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82374
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-82374
```

```
Query Match 7.5%; Score 53.4; DB 9; Length 468;
Best Local Similarity 51.6%; Pred. No. 2.7e-05;
Matches 148; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 142 CATATCAATATATCTGCCGCATCGCCTGTTAGGCTGTTCACATTAATATGAACGTG 201
Db 139 CATACTAATTTTGTGTTTTCCTAATGCTCCAGAGTTCATGTACAGCAAAACGGCGTGCA 198
QY 202 GCTATGCCCTTCATGGTTTGATATTATG---GGCTTTCCACAGATTCACAGGAGGATGAA 258
Db 199 TTGATGCCCTGCTTGGTTTGACATCTTGGAAATGGGATCCTAGTTTTCACAAAGTTGACAT 258
QY 259 TCTGGATTAAACAGCAGCAGCAAGAAATATAAAGCTTTGATTTGATCAAGAAAGTGAAGAT 318
Db 259 GACGGTTTATGAATCTTTGAAATTCCTATGAAGACGGTTAAGCAAGAAATGATATAA 318
QY 319 GGCATTTCTCTTAAACAGAAATATTTTGGAGGGTTTCTCAGGAGGAGCTTTATCTTTA 378
Db 319 GGAATTTAAACCGGAGCAGATTAATTCGAGGTTTCTCTCAGGTTGCCGCAATTAGCTCTC 378
QY 379 TATACAGCCCTTACACACAGCAAGAACTGGCAGGTGTCACTGCACCT 425
Db 379 GCAACATCATGTTACTTTTACCATGGAAAAATCCGGTGGTATAGTAGTCTCT 425
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```
RESULT 13
US-10-932-182A-82374
; Sequence 82374, Application US/10932182A
; Publication No. US20060046253A1
```

GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 82374
LENGTH: 468
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-82374

Query Match 7.5%; Score 53.4; DB 9; Length 468;
Best Local Similarity 51.6%; Pred. No. 2.7e-05;
Matches 148; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 142 CATATCAATATATCTGCCGCGATCGCTGTAGCCCTGTACATTAATATGAACGNG 201
DB 139 CATACTAATTTTGTCTTCTTAATGCTCCAGAGCTTCATGTGACAGCAAAACGGCGTGCA 198

QY 202 GCTATGCCCTTCATGGTTTGATATTATG---GCTTTTACCAGATTTCACAGGAGGATGAA 258
DB 199 TTGATGCCCTGTGGTTTGACATCTTGAATGGATCGTCTAGTTTTCACAAAGTTGACAGT 258

QY 259 TCTGGATTAACAGCAGCAGCAAGAAATATAAAGCTTTGATTGATCAAGAGTGAAGAAAT 318
DB 259 GACGGTTTATGAATTCCTTGAATTCATAGAAAGACGGTTAAGCAAGAAATTGATAAA 318

QY 319 GCATTCCTCTTAACAGAAATTTTGGAGGGTTTCTCAGGAGGAGCTTTATCTTTA 378
DB 319 GGAATTAACCGAGCAGAGATTTATTCGAGGTTTCTCAGGAGTCCCGCATTTAGCTCTC 378

QY 379 TATAGTCCCTTACCACAGCAGCAAACTGGCAGGTGTCACTGCAC 425
DB 379 GCAACATGATTTACTTTTACATGGAATAATCGGTGATATAGTCTCT 425

RESULT 14
US-10-995-561-255
Sequence 255, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 255
LENGTH: 8098
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-255

Query Match 5.3%; Score 37.6; DB 8; Length 8098;
Best Local Similarity 55.8%; Pred. No. 5.2;
Matches 70; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY 569 AAACATTTGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATGATGCACAGTT 628
DB 1981 AAATCTGGGCACCTAATAGACAGCTTACCCTCTCCAGCCATTGATCATGAGCAGCTCAGGC 2040

QY 629 CGTGTCAACAGGAAATGTGATGTCAAGCAATTCATGATAAACTCCCTACCTCCCAATTG 688

Db 2041 AGCAACAAGAGGAATGAGGCAATTAAGGGAATCTATTGCTGAACACAAACCTCATATTG 2100

QY 689 ATTGAC 694
Db 2101 ACAAAAC 2106

RESULT 15
US-10-995-561-261
Sequence 261, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 261
LENGTH: 10407
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-261

Query Match 5.3%; Score 37.6; DB 8; Length 10407;
Best Local Similarity 55.6%; Pred. No. 5.9;
Matches 70; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY 569 AAACATTTGGTGAATCCAGCCCAATGTGACCTTTAAACCTATGAAGGTATGATGCACAGTT 628
DB 4480 AAATCTGGGCACCTAATAGACAGCTTACCCTCTCCAGCCATTGATCATGAGCAGCTCAGGC 4539

QY 629 CGTGTCAACAGGAAATGTGATGTCAAGCAATTCATGATAAACTCCCTACCTCCCAATTG 688
DB 4540 AGCAACAAGAGGAATGAGGCAATTAAGGGAATCTATTGCTGAACACAAACCTCATATTG 4599

QY 689 ATTGAC 694
DB 4600 ACAAAAC 4605

Search completed: April 14, 2006, 13:43:08
Job time : 670 secs

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CC regulate the multifunctional lysophospholipids; increased levels of
 CC lysophospholipids are associated with a host of diseases. The enzyme is
 CC widely distributed in almost all tissues, although levels vary. LysoPLA
 CC cDNA (see AAH26336) was obtained by PCR amplification of human brain cDNA
 CC using primers (see AAH26337-38) based on human sequences identified by
 CC database screening using a mouse sequence. The PCR product was expressed
 CC in *Escherichia coli* BL21 (DE3) cells using vector pET28a(a). The
 CC recombinant LysoPLA protein, which included an N-terminal 6His tag and
 CC thrombin cleavage site, was recovered on an Ni-NTA column. Kinetic
 CC analysis showed that human LysoPLA displays apparent co-operativity and
 CC surface dilution kinetics. The recombinant LysoPLA can be used in the
 CC treatment of disease states having elevated concentrations of
 CC lysophospholipids, such as atherosclerosis, hyperlipidaemia, lethal
 CC dysrhythmia in myocardial ischaemia and segmental demyelination of
 CC peripheral nerves. The LysoPLA may be supplied to the enzyme-deficient
 CC patient by infusion or by gene therapy (both claimed). Also claimed is a
 CC method of inhibiting human brain LysoPLA activity using methyl
 CC arachidonyl fluorophosphates

XX Sequence 230 AA;

Query Match 100.0%; Score 1208; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 8.5e-124;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 QY 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSITYALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSITYALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230
 DB 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230

RESULT 2
 AAY09531
 ID AAY09531 standard; protein; 230 AA.

XX AC AAY09531;

XX 19-JUL-1999 (first entry)

XX Human lysophospholipase extended NHLP.

XX Human; lysophospholipase; NHLP; cell proliferation; arteriosclerosis;
 KW atherosclerosis; bursitis; cirrhosis; hepatitis; myelofibrosis;
 KW mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
 KW polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;
 KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;
 KW immune response; ankylosing spondylitis; autoimmune haemolytic anaemia.

XX Homo sapiens.

XX WO9849319-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US008782.

XX 29-APR-1997; 97US-00844120.

XX 12-FEB-1998; 98US-00022940.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Shah P, Murry LE;

XX

WP1: 1999-326512/27.

DR N-PSDB; AAX56267.

XX New human lysophospholipase (NHLP) polypeptides and polynucleotides which
 PT identify and encode NHLP.

XX Claim 1; Fig 2; 66pp; English.

XX The present sequence is human lysophospholipase (NHLP). The present
 CC invention also describes a method for treating or preventing a disorder
 CC of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
 CC paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis,
 CC primary thrombocytopenia, and cancers), inflammation (e.g. Addison's
 CC disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
 CC disorder of the immune response (e.g. AIDS, allergies, ankylosing
 CC spondylitis, autoimmune haemolytic anaemia) by administering an
 CC antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,
 CC complementary sequences or vectors may be administered in combination
 CC with other therapeutic agents. Antibodies which specifically bind to NHLP
 CC may be used for the diagnosis of disorders characterized by expression of
 CC NHLP or in assays to monitor patients being treated with NHLP or
 CC agonists. The polynucleotides (PNA) encoding NHLP or fragments may be
 CC used therapeutically. In one aspect, the complement of the
 CC polynucleotides may be used where it would be desirable to block the
 CC transcription of the mRNA. Complementary molecules may be used to
 CC modulate NHLP activity or to achieve regulation of gene activity.
 CC Diagnostically, the PNA may be used to detect and quantitate gene
 CC expression in biopsied tissues in which expression of NHLP may be
 CC correlated with disease

XX Sequence 230 AA;

Query Match 99.7%; Score 1204; DB 2; Length 230;
 Best Local Similarity 99.6%; Pred. No. 2.3e-123;
 Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

DB 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSITYALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180

DB 121 GGALSITYALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230

DB 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230

RESULT 3

AU85134

ID AU85134 standard; protein; 230 AA.

XX AC AU85134;

XX 08-MAY-2002 (first entry)

XX Human lysophospholipase I #2.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipaeamic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.

XX Homo sapiens.

XX WO200210185-A1.

```

XX PD 07-FEB-2002.
XX XX
XX PF 20-JUL-2001; 2001WO-US022975.
XX PR 31-JUL-2000; 2000US-00629645.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Wyatt JR;
XX XX
XX WPI; 2002-188720/24.
XX DR N-PSDB; ABK37045.
XX XX
XX Novel antisense compound useful for treating inflammation,
XX PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
XX PT myocardial ischemia, inhibits lysophospholipase I.
XX PS Disclosure; Page 94-95; 131pp; English.
XX XX
XX The invention relates to an antisense compound (I) 8-30 nucleobases in
XX CC length targeted to a nucleic acid molecule encoding lysophospholipase I
XX CC (II), where (I) specifically hybridises with and inhibits the expression
XX CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
XX CC tissues, and for treating a human having a disease or condition
XX CC associated with Lysophospholipase I e.g. inflammation, hyperlipidaemia,
XX CC and cardiovascular disorders such as atherosclerosis and myocardial
XX CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
XX CC useful for distinguishing functions of various members of a biological
XX CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
XX CC represent lysophospholipase I amino acid sequences of the invention
XX CC
XX SQ Sequence 230 AA;
XX
Query Match 99.7%; Score 1204; DB 5; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLMNVAMPSPFDIIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPFDIIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSlyTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSlyTALTTOQKLAGVTALSCWLPRLASFPQGPFGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 4
AAU85132
ID AAU85132 standard; protein; 230 AA.
XX AC AAU85132;
XX XX
XX 08-MAY-2002 (first entry)
XX DE Human lysophospholipase I #1.
XX XX
XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
XX KW antilipaeic; cardiant; lysophospholipase I; inflammation; ischaemia;
XX KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
XX KW antisense gene therapy.
XX XX
XX Homo sapiens.
XX OS
XX WO200210185-A1.
XX PN

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XX PD 07-FEB-2002.
XX XX
XX PF 20-JUL-2001; 2001WO-US022975.
XX PR 31-JUL-2000; 2000US-00629645.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Wyatt JR;
XX XX
XX WPI; 2002-188720/24.
XX DR N-PSDB; ABK37030.
XX XX
XX Novel antisense compound useful for treating inflammation,
XX PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
XX PT myocardial ischemia, inhibits Lysophospholipase I.
XX PS Disclosure; Page 88-89; 131pp; English.
XX XX
XX The invention relates to an antisense compound (I) 8-30 nucleobases in
XX CC length targeted to a nucleic acid molecule encoding lysophospholipase I
XX CC (II), where (I) specifically hybridises with and inhibits the expression
XX CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
XX CC tissues, and for treating a human having a disease or condition
XX CC associated with Lysophospholipase I e.g. inflammation, hyperlipidaemia,
XX CC and cardiovascular disorders such as atherosclerosis and myocardial
XX CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
XX CC useful for distinguishing functions of various members of a biological
XX CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
XX CC represent lysophospholipase I amino acid sequences of the invention
XX CC
XX SQ Sequence 230 AA;
XX
Query Match 99.7%; Score 1204; DB 5; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLMNVAMPSPFDIIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPFDIIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSlyTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSlyTALTTOQKLAGVTALSCWLPRLASFPQGPFGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 5
ABR54198
ID ABR54198 standard; protein; 230 AA.
XX AC ABR54198;
XX XX
XX 23-JUN-2003 (first entry)
XX DE Human NOV7c protein SEQ ID NO:64.
XX XX
XX Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
XX KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
XX KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
XX KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaeic;
XX KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
XX KW congenital heart defect; aortic stenosis; valve disease; transplantation;
XX KW tubercous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
XX KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;

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XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 230 AA;

Query Match 99.7%; Score 1204; DB 7; Length 230;
 Best Local Similarity 99.6%; Pred. No. 2.3e-123;
 Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
 DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
 QY 61 VTLMNNVAMPSWFDIIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLMNNVAMPSWFDIIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSILYALTTOQKLAGVTALSCWPLPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSILYALTTOQKLAGVTALSCWPLPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230
 DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230

RESULT 7
 ADD45662
 ID ADD45662 standard; protein; 230 AA.

XX ADD45662;

XX 29-JAN-2004 (first entry)

XX Human Protein NP_006321, SEQ ID NO 11330.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 WIPI: 2003-268312/26.
 DR GENBANK; NP_006321.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 230 AA;

Query Match 99.7%; Score 1204; DB 7; Length 230;
 Best Local Similarity 99.6%; Pred. No. 2.3e-123;
 Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
 DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
 QY 61 VTLMNNVAMPSWFDIIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLMNNVAMPSWFDIIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSILYALTTOQKLAGVTALSCWPLPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSILYALTTOQKLAGVTALSCWPLPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230
 DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230

RESULT 8
 ABM80990
 ID ABM80990 standard; protein; 230 AA.

XX

AC	ABM80990;	
XX	18-NOV-2004 (first entry)	
DT		
DE	Tumour-associated antigenic target (TAT) polypeptide PRO59230, SEQ.2551.	
XX		
DE	Tumour-associated antigenic target; TAT; human; overexpression; cancer;	121
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;	121
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;	121
KW	central nervous system cancer; bladder cancer; pancreatic cancer;	121
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;	121
KW	chromosome identification; chromosome mapping; gene mapping;	121
KW	gene therapy; cytostatic.	121
XX		
OS	Homo sapiens.	181
XX		
XX	WO2004030615-A2.	181
PN		
XX	15-APR-2004.	181
PD		
XX	29-SEP-2003; 2003WO-US028547.	181
PF		
XX	02-OCT-2002; 2002US-0414971P.	181
PR		
XX	(GETH) GENENTECH INC.	181
XX		
PA		
XX		
PI	Wu TD, Zhang Z, Zhou Y;	181
XX		
XX	WPI; 2004-347921/32.	181
DR		
DR	N-PSDB; ACN38804.	181
XX		
XX	New tumor-associated antigenic target polypeptides and nucleic acids,	181
PT	useful in preparing a medicament for treating or detecting a	181
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or	181
PT	prostate cancer or tumor.	181
XX		
PS	Claim 12; SEQ ID NO 2551; 7273pp; English.	181
XX		
XX	The invention relates to human tumour-associated antigenic target (TAT)	181
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are	181
CC	overexpressed in cancer tissues compared to normal tissues, and may thus	181
CC	serve as effective targets for the diagnosis and treatment of cancer in	181
CC	mammals. The invention also relates to nucleic acid and polypeptide	181
CC	sequences at least 80% identical to the TAT nucleic acids and	181
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic	181
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic	181
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a	181
CC	TAT polypeptide; and methods and compositions for the treatment or	181
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,	181
CC	antibodies, antagonists, binding molecules and compositions are useful	181
CC	for diagnosing or treating a cell proliferative disorder associated with	181
CC	increased TAT expression, particularly cancers such as breast cancer,	181
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder	181
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central	181
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be	181
CC	used as hybridisation probes, in chromosome and gene mapping, in	181
CC	chromosome identification and in gene therapy. The present sequence	181
CC	represents a TAT polypeptide of the invention	181
XX		
SQ	Sequence 230 AA;	181
	Query Match 99.7%; Score 1204; DB 8; Length 230;	
	Best Local Similarity 99.6%; Pred. No. 2.3e-123;	
	Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP 60	1
Db	1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP 60	1
QY	61 VTLNMNVMPSPWDIIGLSPDSQDESGIKQAAENIKALIDQVKNIGIPSNRIILGFSQ 120	61
Db	61 VTLNMNVMPSPWDIIGLSPDSQDESGIKQAAENIKALIDQVKNIGIPSNRIILGFSQ 120	61

QY	121	GGALSXYTALTQQKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
Db	121	GGALSXYTALTQQKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY	181	FGSLTVEKLTILVNPANVTFTYEGMHSSCOQENMDVKQFIDKLLPPID 230
Db	181	FGSLTVEKLTILVNPANVTFTYEGMHSSCOQENMDVKQFIDKLLPPID 230
RESULT 9		
AAB53451		
ID	AAB53451	standard; protein; 263 AA.
XX		
AC	AAB53451;	
XX		
DT	09-MAR-2001 (first entry)	
XX		
DE	Human colon cancer antigen protein sequence SEQ ID NO:991.	
XX		
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;	
KW	identification; cytostatic; cardioactive; neuroprotective; vulnerary;	
KW	immunomodulatory; muscular; gynaecological; gastrointestinal;	
KW	nephrotropic; antiinfective; antibacterial; gene therapy; wound;	
KW	neural disorder; immune system disorder; muscular disorder;	
KW	reproductive disorder; gastrointestinal disorder; renal disorder;	
KW	infectious disease; cardiovascular disorder.	
XX		
OS	Homo sapiens.	
XX		
XX	WO200055351-A1.	
PN		
XX	21-SEP-2000.	
PD		
XX		
PF	08-MAR-2000; 2000WO-US005883.	
XX		
PR	12-MAR-1999; 99US-0124270P.	
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
XX		
PI	Rosen CA, Ruben SM;	
XX		
XX	WPI; 2000-587534/55.	
DR	N-PSDB; AAC98208.	
XX		
PT	Colon cancer associated gene sequences, referred to as colon cancer	
PT	antigens, useful for the treatment, prevention, and diagnosis of colon	
PT	disorders such as colon cancer.	
XX		
PS	Claim 11; Page 1568-1569; 2104pp; English.	
XX		
CC	AAC97991 to AAC98763 encode the human colon cancer associated proteins,	
CC	called human colon cancer antigens, given in AAB53234 to AAB54006. The	
CC	human colon cancer antigens can have cytostatic, cardioactive, muscular;	
CC	neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and	
CC	vulnerary, nephrotropic, antiinfective and antibacterial activities, and	
CC	can be used in gene therapy. The colon cancer antigen polynucleotides,	
CC	proteins and antibodies to the proteins are useful for the prevention,	
CC	treatment and diagnosis of colon disorders, such as colon cancer. The	
CC	polynucleotides may be used in diagnostics and research, such as for	
CC	chromosome identification, and as hybridisation probes. The proteins may	
CC	also be used to prevent diseases such as neural disorders, immune system	
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal	
CC	disorders, wounds, renal disorders, infectious diseases, and	
CC	cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent	
CC	sequences used in the exemplification of the present invention	
XX		
SQ	Sequence 263 AA;	
	Query Match 99.7%; Score 1204; DB 3; Length 263;	
	Best Local Similarity 99.6%; Pred. No. 2.8e-123;	
	Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP 60	1

Db 34 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 93
QY 61 VTLLNNVAMPSPWFDIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 94 VTLLNNVAMPSPWFDIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 153
QY 121 GGALSILYALTATTOQKLAGVTALSCWPLPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 154 GGALSILYALTATTOQKLAGVTALSCWPLPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 213
QY 181 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
Db 214 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 263

RESULT 10
ABG07277
ID ABG07277 standard; protein; 275 AA.
XX
AC ABG07277;
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #7268.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR N-PSDB; AAS71484.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 37636; 103pp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 275 AA;
Query Match 99.7%; Score 1204; DB 4; Length 275;
Best Local Similarity 99.6%; Pred. No. 3e-123; 1; Indels 0; Gaps 0;
Matches 229; Conservative 0; Mismatches 1;
QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 46 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 105
QY 61 VTLLNNVAMPSPWFDIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 106 VTLLNNVAMPSPWFDIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 165
QY 121 GGALSILYALTATTOQKLAGVTALSCWPLPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 166 GGALSILYALTATTOQKLAGVTALSCWPLPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 225
QY 181 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
Db 226 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 275

RESULT 11
ABR54196
ID ABR54196 standard; protein; 230 AA.
XX
AC ABR54196;
DT 23-JUN-2003 (first entry)
XX
DE Human NOV7a protein SEQ ID NO:60.
XX
KW Human; NOVX; antiatherosclerotic; hypotensive; cardiac; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipemic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberosus sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X.
XX
OS Homo sapiens.
XX
PN WO2003023001-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028538.
XX
XX 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318184P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 14-DEC-2001; 2001US-0341144P.

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PR 26-FEB-2002; 2002US-0359599P.
PR 05-MAR-2002; 2002US-0361663P.
PR 03-MAY-2002; 2002US-0377908P.
PR 17-MAY-2002; 2002US-0381483P.
PR 29-MAY-2002; 2002US-0383863P.
PR 02-JUL-2002; 2002US-0393332P.
PR 17-JUL-2002; 2002US-0396412P.
PR 13-AUG-2002; 2002US-0403517P.
PR 06-SEP-2002; 2002US-00236417.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI Kekuda R, Khrantsov NV, Leach MD, Lepley DM, Li L, Liu X;
PI Malyankar UM, Miller CE, Ooi T, Padigar M, Patturajan M;
PI Pena CE, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
PI Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong M;
XX
XX WPI; 2003-313241/30.
DR N-PSDB; ACC62265.
XX
XX Novel human proteins and nucleic acid encoding the proteins, useful for
PT diagnosis, treatment and prevention of disorders involving the human
PT protein or nucleic acid e.g. cardiac and neurological disorders.
XX
XX Claim 1; Page 129; 460pp; English.
XX
CC The present invention describes isolated human NOVX proteins, where X is
CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiac,
CC hypotensive, dermatological, anorectic, immunosuppressive, cardiac,
CC antidiabetic, antifertility, haemostatic, antiinflammatory, cytostatic,
CC antiasthmatic, metabolic, immunomodulator, neuroprotective, nontropic,
CC antiparkinsonian and antilipemic activities, and can be used in gene
CC therapy. NOVX proteins are useful for treating or preventing a pathology
CC associated with a NOVX protein in humans and for treating a syndrome
CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberosclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterine cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human trypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
XX Sequence 230 AA;
SQ
Query Match 95.4%; Score 1153; DB 6; Length 230;
Best Local Similarity 94.8%; Pred. NO. 9.4e-118;
Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MCGNNMSTLPAIVPAARAKATAAIVFLHGLDGTGCHGWAFAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTLPTITVPAAPKATTEVIFLHGLDGTGCHGWAFAFAGITSSHIKYICPHAPVRP 60
QY 61 VTLLNMVAMPSFDDIIGLSPDSDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMVAMPSFDDIIGLSPDSDESGIKQAQNIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYLTATTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYLTATTHOKLAGVTALNCWLPWASFPQGPFGGANRDISILQCHGDCDPLVPLM 180

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QY 181 FGSLTVEKLTLPANPANTVFTKTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTLPANPANTVFTKTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
RESULT 12
ADE47694
ID ADE47694 standard; protein; 230 AA.
XX
XX ADE47694;
XX
XX 29-JAN-2004 (first entry)
XX Human NOV18a protein SEQ ID NO:56.
XX human; cardiac; antiarteriosclerotic; hypotensive; immunosuppressive;
KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;
KW anti-HIV; antiasthmatic; antibacterial; virucide; neuroprotective;
KW nontropic; antiparkinsonian; antilipemic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003076642-A2.
XX
XX 18-SEP-2003.
XX
XX 02-AUG-2002; 2002WO-US024459.
XX
XX 02-AUG-2001; 2001US-0309501P.
XX 03-AUG-2001; 2001US-0310291P.
XX 08-AUG-2001; 2001US-0310951P.
XX 09-AUG-2001; 2001US-0311292P.
XX 13-AUG-2001; 2001US-0311979P.
XX 14-AUG-2001; 2001US-0312203P.
XX 17-AUG-2001; 2001US-0313156P.
XX 17-AUG-2001; 2001US-0313201P.
XX 20-AUG-2001; 2001US-0313702P.
XX 21-AUG-2001; 2001US-0314031P.
XX 23-AUG-2001; 2001US-0314466P.
XX 28-AUG-2001; 2001US-0315403P.
XX 29-AUG-2001; 2001US-0315853P.
XX 31-AUG-2001; 2001US-0316508P.
XX 21-SEP-2001; 2001US-0323936P.
XX 03-DEC-2001; 2001US-0338078P.
XX 05-FEB-2002; 2002US-0354655P.
XX 05-MAR-2002; 2002US-0361764P.
XX 19-APR-2002; 2002US-0373825P.
XX 15-MAY-2002; 2002US-0380971P.
XX 16-MAY-2002; 2002US-0380980P.
XX 28-MAY-2002; 2002US-0381039P.
XX 29-MAY-2002; 2002US-0383761P.
XX 01-AUG-2002; 2002US-0383887P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Zerhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;
PI Pena CE, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
PI Boldog FL, Padigar M, Smithson G, Shenoy SG, Ji W, Gorman L;
PI Vernet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
PI Burgess CE, Khrantsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;
PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA;
PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;
PI Taupier RJ, Catterton E;
XX
XX WPI; 2003-779062/73.
DR N-PSDB; ADE47693.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes,
PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
PT or pharmacogenomics.

```

XX Claim 1; SEQ ID NO 56; 562bp; English.

XX The invention relates to a novel (NOVX) human polypeptide. A polypeptide

XX of the invention has cardiac, antiarteriosclerotic, hypotensive,

XX immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,

XX haemostatic, anti-HIV, antisthmatic, antibacterial, virucide,

XX neuroprotective, neurotropic, antiparkinsonian, and antilipase activity.

XX A polynucleotide encoding a polypeptide of the invention may have a use

XX in gene therapy, and as a vaccine. A polypeptide of the invention is

XX useful in the manufacture of a medicament for treating a syndrome

XX associated with a human disease, the disease selected from a pathology

XX associated with the polypeptide. These may also be used in diagnosing,

XX treating or preventing NOVX-associated disorders such as cardiomyopathy,

XX atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

XX haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,

XX multiple sclerosis, infections, anorexia, cancer-associated cachexia,

XX neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's

XX disease), haematopoietic disorders, dyslipidaemias and other wasting

XX disorders associated with chronic diseases. The nucleic acids are also

XX used as hybridisation probes, in chromosome mapping, tissue typing,

XX preventive medicine, and pharmacogenomics. The polypeptides are also

XX useful as vaccines. The present sequence represents a NOVX polypeptide of

XX the invention.

SQ Sequence 230 AA;

Query Match 95.4%; Score 1153; DB 7; Length 230;

Best Local Similarity 94.8%; Pred. No. 9.4e-118; Indels 0; Gaps 0;

Matches 218; Conservative 4; Mismatches 8;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHCWAFAFAGIRSHIKYICPHAPVRP 60

DB 1 MCGNNMSTPLPAIVPAARKATTEVFLHGLGDTGHCWAFAFAGIRSHIKYICPHAPVRP 60

QY 61 VTLLNNVAMPSPDITGLSPDSQDESGIKQAENIKALIDQEVKNGIFSNRIILGGFSQ 120

DB 61 VTLLNNIAMPSPDITGLSPDSQDESGIKQAENIKALIDQEVKNGIFSNRIILGGFSQ 120

QY 121 GGALSILYTTALTTHOKLAGVTALNCWLPPLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180

DB 121 GGALSILYTTALTTHOKLAGVTALNCWLPPLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTLLNPNANVTFTKEGMMHSSCQEMMDVKQFIDKLLPPID 230

DB 181 FGSLTVEKLTLLNPNANVTFTKEGMMHSSCQEMMDVKQFIDKLLPPID 230

RESULT 13

ADJ78964

ID ADJ78964 standard; protein; 230 AA.

XX ADJ78964;

AC ADJ78964;

XX

DT 06-MAY-2004 (first entry)

XX

XX Human NOVX protein Nov18A amino acid sequence.

DE

XX NOVX; cytostatic; antidiabetic; anorectic; cerebroprotective;

XX neuroprotective; antiinflammatory; thyromimetic; cardiac; gene-therapy;

KW antisense-therapy; cancer; diabetes; obesity; endocrine disorder;

KW CNS disorder; cardiovascular disorder; inflammatory disorder;

KW detection assay; screening assay; chromosome mapping; tissue typing;

KW predictive medicine; human; Nov18A.

XX

OS Homo sapiens.

XX

XX US2004014053-A1.

PN

XX 22-JAN-2004.

PD

XX 01-AUG-2002; 2002US-00210130.

PF

XX

PR 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.

PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.

PR 13-AUG-2001; 2001US-0311979P.

PR 14-AUG-2001; 2001US-0312203P.

PR 17-AUG-2001; 2001US-0313156P.

PR 17-AUG-2001; 2001US-0313201P.

PR 20-AUG-2001; 2001US-0313643P.

PR 20-AUG-2001; 2001US-0313702P.

PR 21-AUG-2001; 2001US-0314031P.

PR 23-AUG-2001; 2001US-0314466P.

PR 28-AUG-2001; 2001US-0315403P.

PR 29-AUG-2001; 2001US-0315853P.

PR 31-AUG-2001; 2001US-0316508P.

PR 17-SEP-2001; 2001US-0322716P.

PR 21-SEP-2001; 2001US-0323936P.

PR 03-DEC-2001; 2001US-0338078P.

PR 05-FEB-2002; 2002US-0354655P.

PR 05-MAR-2002; 2002US-0361764P.

PR 19-APR-2002; 2002US-0373825P.

PR 15-MAY-2002; 2002US-0380971P.

PR 16-MAY-2002; 2002US-0380980P.

PR 28-MAY-2002; 2002US-0381039P.

PR 29-MAY-2002; 2002US-0383761P.

PR 29-MAY-2002; 2002US-0383887P.

XX

PA (ZERRH/) ZERHUSEN B D.

PA (PATT/) PATTURAJAN M.

PA (KEKU/) KEKUDA R.

PA (MILL/) MILLER C E.

PA (RIEG/) RIEGER D K.

PA (PENA/) PENNA C E A.

PA (SHIM/) SHIMKETS R A.

PA (LILL/) LI L.

PA (BERG/) BERGHS C.

PA (ZHON/) ZHONG M.

PA (CASN/) CASMAN S J.

PA (VOSS/) VOSS E Z.

PA (BOLD/) BOLDOG F L.

PA (PADI/) PADIGARU M.

PA (SMIT/) SMITHSON G.

PA (JIMW/) JI W.

PA (GORM/) GORMAN L.

PA (VERN/) VERNET C A M.

PA (LEIT/) LEITE M W.

PA (GUOX/) GUO X S.

PA (ANDE/) ANDERSON D W.

PA (SPYT/) SPYTEK K A.

PA (GERL/) GERLACH V.

PA (BURG/) BURGESS C E.

PA (KHRA/) KHRAMTSOV N V.

PA (ORTT/) ORT T.

PA (ELLE/) ELLERMAN K.

PA (RAST/) RASTELLI L.

PA (AGEE/) AGEES M L.

PA (CHAU/) CHAUDHURI A.

PA (CHAN/) CHANT J S.

PA (DIP/) DIPPO V A.

PA (EDIN/) EDINGER S R.

PA (EISE/) EISEN A J.

PA (GANG/) GANGOLLI E A.

PA (GIOT/) GIOT L.

PA (OOIC/) OOI C E.

PA (ROTH/) ROTHENBERG M E.

PA (SPAD/) SPADERNA S K.

PA (HJAL/) HJALT T.

PA (LIUX/) LIU X.

PA (TAUP/) TAUPIER R J.

PA (CATT/) CATTERTON E.

PA (SHEN/) SHENOY S G.

XX

PI Zerhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;

PI Pena CEA, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
PI Boldog PL, Padigaru M, Smithson G, Ji W, Gorman L, Vernet CAM;
PI Leite MW, Guo XS, Anderson DW, Spytek KA, Gerlach V, Burgess CF;
PI Khrantsov NV, Ort T, Ellerman K, Rastelli L, Agee ML, Chaudhuri A;
PI Chant JS, Dipippo VA, Edinger SR, Eisen AJ, Gangolli EA, Giot L;
PI Ooi CE, Rothenberg ME, Spaderna SK, Hjalt T, Liu X, Taupier RJ;
PI Catterton E, Shenoy SG;
XX WPI; 2004-108206/11.
DR N-PSDB; ADJ78963.
XX

XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.

XX Claim 1; SEQ ID NO 56; 250bp; English.

XX This invention relates to a novel isolated NOVX polypeptide comprising a
CC fully defined sequence of, a mature form, one or more conservative
CC substitutions or at least 95% identity to 247 amino acids as given in the
CC specification. The invention may be useful for the development of
CC compounds with a cytostatic, antidiabetic, anorectic, cerebroprotective,
CC neuroprotective, antiinflammatory, thyromimetic or cardiact activity. In
CC addition, the disclosed sequences may prove useful for gene-therapy or
CC antisense-therapy. The invention may be useful for the diagnosis and
CC treatment of disorders associated with aberrant expression or activity of
CC the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine,
CC CNS, cardiovascular and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. The present sequence is that of a human NOVX
CC protein of the invention.

XX SQ Sequence 230 AA;

Query Match 95.4%; Score 1153; DB 8; Length 230;
Best Local Similarity 94.8%; Pred. No. 9.4e-118;
Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLTPVAPRKATTEVIFLHGLGDTGHWAEAFAGIITSSHIKYICPHAPVRP 60
QY 61 VTILNMVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTHQKLAGVTALNCWLPRLWASFPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 14
AAU85133
ID AAU85133 standard; protein; 230 AA.

XX AAU85133;

XX 08-MAY-2002 (first entry)

XX Mouse lysophospholipase I #1.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
KW antilipemic; cardiact; lysophospholipase I; inflammation; ischaemia;
KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
KW antisense gene therapy.
XX Mus musculus.

PN WO200210185-A1.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-US022975.

XX 31-JUL-2000; 2000US-00629645.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2002-188720/24.

XX N-PSDB; ABK37037.

XX Novel antisense compound useful for treating inflammation,
PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
PT myocardial ischemia, inhibits lysophospholipase I.

XX Disclosure; Page 92-93; 131pp; English.

XX The invention relates to an antisense compound (I) 8-30 nucleobases in
CC length targeted to a nucleic acid molecule encoding lysophospholipase I
CC (II), where (I) specifically hybridises with and inhibits the expression
CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
CC tissues, and for treating a human having a disease or condition
CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
CC and cardiovascular disorders such as atherosclerosis and myocardial
CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
CC useful for distinguishing functions of various members of a biological
CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
CC represent lysophospholipase I amino acid sequences of the invention

XX SQ Sequence 230 AA;

Query Match 93.5%; Score 1130; DB 5; Length 230;
Best Local Similarity 91.3%; Pred. No. 3.2e-115;
Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
QY 61 VTILNMVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMVAMPWFDDIIGLSPDQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASFSQGPINSANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMDVKRHFIDKLLPPID 230

RESULT 15
ADD45660
ID ADD45660 standard; protein; 230 AA.

XX ADD45660;

XX 29-JAN-2004 (first entry)

XX Rat Protein NP_037138, SEQ ID NO 11328.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CGI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.

Job time : 198 secs

PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
XX GENBANK; NP_037138.
DR
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 230 AA;

Query Match 93.1%; Score 1125; DB 7; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.le-114;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLDGTGHGWAEPAGIRSSHIKYICPHAPVRP 60
DB 1 MCGNNMSAPVAVVPAARKATAAVIFLHGLDGTGHGWAEPAGIKSKSHIKYICPHAPVMP 60
QY 61 VTLLNMVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMSMMPWFDDIIGLSPDQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYALTTOQKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYALTTOQKLAGVTALSCWLPRLASFQGPPIINSANRDISVLQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTLPANVTFKVEGMHSSQQQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVERLGLNPNVTFKVEGMHSSQQQEMDMVKYFIDKLLPPID 230

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 21:14:16 ; Search time 40 Seconds
(without alignments)
553.246 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTLPAIPAARKA.....CQEMMDVKQFDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510.5	42.3	333	2 T23324	hypothetical prote
2	471	39.0	247	2 T52511	related to lysopho
3	371.5	30.8	224	2 T39158	lysophospholipase
4	356	29.5	227	2 S64955	probable membrane
5	326.5	27.0	224	2 H82658	carboxylesterase x
6	279	23.1	218	2 JU0277	carboxylesterase (
7	274	22.7	215	2 A83163	probable carboxyle
8	272	22.5	218	2 JQ0885	esterase A (EC 3.1
9	271.5	22.5	471	2 T04911	hypothetical prote
10	183	15.1	161	2 C96568	hypothetical prote
11	167.5	13.9	126	2 D96518	protein T256.14 [i
12	164.5	13.6	204	2 S75304	serine esterase -
13	153	12.7	200	2 G96550	hypothetical prote
14	152.5	12.6	207	2 S43880	esterase - Spiruli
15	151	12.5	214	2 AB2195	serine esterase [i
16	149	12.3	197	2 A96568	hypothetical prote
17	147	12.2	197	2 B96568	hypothetical prote
18	147	12.2	241	2 T39231	probable lysophosp
19	124.5	10.3	243	2 G86524	lysophospholipase
20	124.5	10.3	243	2 D72098	serine esterase, p
21	123.5	10.2	305	2 T20470	hypothetical prote
22	120	9.9	304	2 D86998	probable secreted
23	117	9.7	304	2 C70982	probable lpqc prot
24	111	9.2	239	2 F81704	serine esterase, p
25	110.5	9.1	204	2 F83921	hypothetical prote
26	107.5	8.9	395	2 F72424	hypothetical prote
27	103	8.5	319	2 AB1334	hypothetical prote
28	102.5	8.5	215	2 D71634	hypothetical prote
29	101.5	8.4	219	2 A70734	probable cutinase

30	101.5	8.4	243	2 C95908	hypothetical prote
31	101	8.4	378	2 T41456	probable phosphol
32	100.5	8.3	216	2 C97843	serine esterase ho
33	98.5	8.2	240	2 G91045	hypothetical prote
34	98.5	8.2	240	2 C85890	hypothetical prote
35	98	8.1	335	2 T20465	hypothetical prote
36	97.5	8.1	284	2 S17820	protoporphyrin IX
37	97	8.0	433	2 A39556	triacylglycerol li
38	95	7.9	416	2 D70347	cell division prot
39	95	7.9	655	2 T34219	hypothetical prote
40	94	7.8	414	2 S39530	poly(3-hydroxybuty
41	93.5	7.7	240	2 H65022	hypothetical prote
42	92.5	7.7	239	2 A71552	probable lysophosp
43	92	7.6	276	2 A55211	chloride peroxidase
44	92	7.6	656	2 E96713	hypothetical prote
45	91	7.5	250	2 AF1357	hypothetical prote

ALIGNMENTS

RESULT 1

T23324
hypothetical protein K04G2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23324
R;Gardner, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19727
A;Accession: T23324
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-333 <WIL>
A;Cross-references: UNIPROT:Q21224; UNIPARC:UPI000017BA8D; EMBL:Z75712; PIDN:CAB00042.1
A;Experimental source: Clone K04G2
C;Genetics:
A;Gene: CESP:K04G2.5
A;Map position: 1
A;Introns: 8/1; 54/1; 87/1; 165/2; 263/3; 318/3

Query Match	42.3%;	Score	510.5;	DB	2;	Length	333;
Best Local Similarity	49.3%;	Pred. No.	7e-40;				
Matches	106;	Conservative	29;	Mismatches	71;	Indels	9;
Gaps	5;						
QY	11	PAIVPAARKATAAAVIFLHGLGDTGHGWAFAF-AGIRSSHIIKICPHAPVRPVTLMNVAM	69				
Db	119	PSIVSPRGHKGTLLIFLHGLDQGHGWAFAFKTEAKHDNIKFCIPHSSEPPVTLMNGMRM	178				
QY	70	PSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTA	129				
Db	179	PAWFDLFGLDPAQDEQGINRATQVYHQLIDAEVAAGIPASRIAVGVGFSMGALAIYAG	238				
QY	130	LTTQOKLAGVTALSCLWLPASLPQGPFGG--ANRDISILOCHDCDPLVPLMFGSLTVE	187				
Db	239	LTYPQKLGIVGLSFFLQRTKFP-----GSFTANNATPIFLGHGTDPLFLPFGQMSQ	294				
QY	188	KLKTLVNPANVTFTYEGHMHSSCCQCEMMDVKQFI	222				
Db	295	YIKKF-NP-KVELHYRGMQHSSCGEMRDVKTFL	327				

RESULT 2

T52511
related to lysophospholipase [imported] - Neurospora crassa
N;Alternate names: protein B2J23.70
C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
R;Schulte, U.; Align. V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, September 2000
A;Reference number: Z26053
A;Accession: T52511

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 [SCH]
A;Cross-references: UNIPROT:Q9HFJ5; UNIPARC:UPT000001796CD; EMBL:AL442164; GSPDB:GN000116;
A;Experimental source: BAC clone B2J23; strain OR74A
C;Genetics:
A;Gene: NCSP:B2J23.70
A;Map position: 6
A;Introns: 85/2; 212/2

Query Match	39.0%;	Score 471;	DB 2;	Length 247;
Best Local Similarity	42.4%;	Pred. No. 2.3e-36;		
Matches	98;	Conservative 40;	Mismatches 79;	Indels 14; Gaps 4;
Qy	11	PAIVPAARKATAAAVIFHGLGDTGHWAEAFAGIRS----	SHIKYICPHAPVRVPTLNMN	66
Db	9	PLLVPAVARHTATVIFHGLGDTGHWASAVEQWRRRORLDEVKFLPAHRSIPTANWG		68
Qy	67	VAMPSWEDIIGLSPDS-----QEDSSGIKQAAENKALIDQVKNGIPSNRIILGGFS		119
Db	69	MKMPGWYDIVSLPTYSVAEALRRNEDEAGILTSQAYFHLIQKEIDSGIPADRIVIGFS		128
Qy	120	QGGALSIVTALTTOOKLAGVTALSCWLPRLASLPQ-GPIGGANRDISILOCHGDCDPLVP		178
Db	129	QGGANGVLPSGLTACKLGIATLSYLLLSLKFAELVPKPFNKETPLFMAHGADPVVN		188
Qy	179	LMFGLSLTVEKILKTLVNPANVTFTKTYEGNMHSSCQOEMMDVMVKQFIDKLLPPI		229
Db	189	YKLGTMTRDLLEKEM--GYNVKFTTYPGNGHSGACLEELDAIEDFTLERLPKV		237

RESULT 3
T39158
lysophospholipase - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39158
E:McLean, J.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21831
A:Accession: T39158
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-224 <MCL>
A:Cross-references: UNIPROT:O42981; UNIPARC:UPI000006AD33; EMBL:AL021817; PIDN:CAAL17025
A:Experimental source: strain 972h; cosmid c8E11
C:Genetics:
A:Gene: SPDB:SPAC8E11.04c
A:Map position: 1
A:Introns: 25/1: 53/2: 69/2: 118/1

Query Match	30.8%;	Score 371.5;	DB 2;	Length 224;
Best Local Similarity	39.9%;	Pred. NO. 4e-27;		
Matches	85;	Conservative 41;	Mismatches 72;	Indels 15; Gaps 6
Qy	21	TAAVIFLHGLGDTGHW--AAFAPIGSSHKYICHPVRPVTNNVAMPWFWDIIG	77	
Db	17	TATVIFLHGLGDSGGCFMANTWSNFK--HKWIFNAPIPVTVNNGMKPAYDIYS	74	
Qy	78	LSPDSQDESGIKQAAENKALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTYYQOKLA	137	
Db	75	FADMKREDENGILRSAGQLHLLIDAEALGIPSDRILIGGFSQGGCMVSLYAGLTPYKRLA	134	
Qy	138	GVTALSCWLPARASLPQGPFGGANDRISIOCHGDCDPLVPLMFQSLTWVKLKTILVNPAN	197	
Db	135	GIMGHSGFPLASKEPSPA--LSRVAKIEIPILTYTETEDFIVPSVLSSASA---LYLIN--N	188	
Qy	198	VTFK---TYEGMMHSSCQEQEMVMVQKFDKLL	226	
Db	189	LOLKCLDRPFGDAHLSLSESPFAMKYFTQTVI	221	

RESULT 4

S64955
probable membrane protein YJR118c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein U2955
C;Species: *Saccharomyces cerevisiae*
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: S64955; S69406
R;Verhaesselt, P.; Voet, M.; Voickaert, G.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64943
A;Accession: S64955
A;Molecule type: DNA
A;Residues: 1-227 <VER>
A;Cross-references: UNIPROT:Q12354; UNIPARC:UPI000006C16B; EMBL:Z73290; NID:gl1
R;Verhaesselt, P.; Voickaert, G.
submitted to the EMBL Data Library, September 1995
A;Reference number: S69393
A;Accession: S69406
A;Molecule type: DNA
A;Residues: 1-227 <VSW>
A;Cross-references: UNIPARC:UPI000006C16B; EMBL:X89514; NID:gl1297019; PID:e198
C;Genetics:
A;Cross-references: SGD:S0004108
A;Map position: 12R
C;Keywords: transmembrane protein #
C;136-152/Domain: transmembrane #status predicted <TWM>

Query Match	29.5%	Score 356;	DB 2;	Length 227;
Best Local Similarity	37.4%;	Pred. NO. 1.2e-25;		
Matches 82; Conservative	29;	Mismatches 90;	Indels 18;	Gaps 4
Qy	20	ATAAVIFLHGLGDTGCHGWA-----BAFAGIRSHIKYICPHAPVRVPTILMNVA	68	
Db	13	ARQTIIIFLHGLGDTGSGWGFLAQYIQQORDPAF-----QHTNFVFPNAPELHVTGTANGGAL	67	
Qy	69	MPSWFDIIGLSPD--SQEDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGNLSLY	127	
Db	68	MPAWFDILEWDPSPFSKVDSDGFMNLSNIEKTVKQEIIDKGIKPEQIIIGGFSQGGNLSLY	127	
Qy	128	TALTTQQKLAGVTALSCWLPURASLPQGPFGIGANRDISLQCHGCDPLPVLPMFGSLTVE	187	
Db	128	TSVTLPWKIGIGIVALSGFCSIPGLIKQHK-NGINVKPTIFHCHGDMDPVVPICGLGKAKQ	186	
Qy	188	KLKTLVNPANPTFTYEGMMHSSCQEQEMDMVKQFIDKLL	226	
Db	187	FYQDSCEITONYEFKVKYKGMMAHSTVPDELEDLASFIKKSLL	225	

RESULT 5
H82658 carboxylesterase XF1624 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82658
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleot
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82658
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <SIW>

A,Residues: 1-224 <SIM>
A,Cross-references: UNIPROT:C9PCV0; UNIPARC:UPI00000C27A6; GB:AE003989; GB:AE050
A,Experimental source: strain 9A5C
R,Impson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares
B,iones, M.R.S.; Bueno, M.R.F.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.;
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.F.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.; Fraga, J.S.; Franca, S.C.; Franco, M.
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.;
A,Authors: Martins, E.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyai

probable carboxylesterase PA3859 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83163
C:R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Residues: 1-215 <STO>

C;Genetics:

Query Match 22.7%; score 2/4; DB 2; length 215;

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DB I MSEFL---ILUAFENADACTIWTUOGLORDKIDAL VAREHQVIVELZ ANI LEL Q-TH Q-TH-1

16

[illegible]

182 GSI.TVEKI.KT.I.VNPANVT.EKTYEGMMHSSCOEMMDVKOFIDKLL 226

590885

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C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
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submitted to JIPID, March 1991

A;Molecule type: DNA

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[illegible]

Matches	72	Conservative	41	Mismatches	98	Indels	8	Gaps	5
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[illegible]

69 MPSWFDIIGLSPDSQDEDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLEYI 128

124 AFRKWEGLGGVIALSIYAFIFDNDLQ--LSASQKRFELDCTHQYIDEVQNAHQKSRIL 101

A;Cross-references: UNIPROT:P73192; UNIPARC:UPI00000D338C; EMBL:D90904; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 13.6%; Score 164.5; DB 2; Length 204;
Best Local Similarity 28.7%; Pred. No. 7.7e-08;
Matches 62; Conservative 41; Mismatches 88; Indels 25; Gaps 10;

QY 9 PLPAIVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRPVTLMNVVA 68
DB 11 PDPAVTPT--DSSYLLVMLHGWGADARDLSLAPMLDLPNYQWRVFNWAFTHPQIPQGRA 68
QY 69 MFSWFDIIGLSDSDSGIQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSIX 127
DB 69 ---WYDL-----ESQNF-GLAQAQGLRAYLLGLAEETGIPLARTILGGFSQGGAMALD 119
QY 128 TALTTOQKLAGVTALSCWPLR-ASLPQGPPIGGANRDISILOCHGDCDPLVPLMFGSLTV 186
DB 120 VGLTL--PLAKFSLSGYLHFPESQPA-----IAPILLHGTEDPVPLRMAQQA 170
QY 187 EKLKTLVNPANVTFTYEGMHSSCOQEMMDVKQFI 222
DB 171 AELESI--GASVEYQEPF-MGHAIPPMALARKSFL 203

RESULT 13

G96550
hypothetical protein Film15.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96550
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
aneen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Liu, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurob, J.S.; Mafti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <STO>
A;Cross-references: UNIPROT:Q9SYD1; UNIPARC:UPI00000A181C; GB:AE005173; NID:g4836939; P
C;Genetics:
A;Gene: Film15.15
A;Map position: 1

Query Match 12.7%; Score 153; DB 2; Length 200;
Best Local Similarity 28.7%; Pred. No. 8.9e-07;
Matches 43; Conservative 30; Mismatches 53; Indels 24; Gaps 7;

QY 13 IVPAAKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRPVTLMNVAM--- 69
DB 30 VTPARH-QATIVLHDLNESGYDSBELVKSFLYVNVKICPSSP-----LISNVFGGA 83
QY 70 --PSWFDIIGLS---PDSQDESGIQAENIKALIDQEVKNGIPSNRIILGGFSQGGAL 124
DB 84 PARAWFKVNEFMRPDPYEME-GLKNSAAHVAGLLKNPENVMKG-----VAGYGIGGAL 138
QY 125 SLYTAL-----TTQOKLAGVTALSCWPLR 149
DB 139 ALHIATCYALGSPFIQIRAVGVINCWLPNR 168

RESULT 14

S43880
esterase - Spirulina platensis
C;Species: Spirulina platensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S43880

R;Salvi, S.; Trinei, M.; Lanfalconi, L.; Pon, C.L.

Mol. Gen. Genet. 243, 124-126, 1994
A;Title: Cloning and characterization of the gene encoding an esterase from Spirulina p
A;Reference number: S43880; MUID:94247351; PMID:8190066

A;Accession: S43880
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-207 <SAL>

A;Cross-references: UNIPROT:Q53415; UNIPARC:UPI00000B29D2; GB:S70419; NID:g546788; PIDN

Query Match 12.6%; Score 152.5; DB 2; Length 207;
Best Local Similarity 29.4%; Pred. No. 1e-06;
Matches 62; Conservative 28; Mismatches 88; Indels 33; Gaps 10;

QY 24 VIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRPVTLMNVAMP---SWFDIIGLSP 80
DB 20 IIFLHGWGANCBDLTFAPMLRLPNYWFEPFPAFF-----PHPOVPGGRAWYAL----- 68
QY 81 DSOEDSGIQAENIKALIDQ-----EVKNGIPSNRIILGGFSQGGALSXYTALTTOQKL 136
DB 69 ETQEYE-GIBESREK---LIDMLNIAQTGTTPORTILGGFSQGGAMTFDVGR--MGF 122
QY 137 AGVTALSCWPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLMFGSLTVKLTALVNP 196
DB 123 AGLIVLSGYLHFKPEPQOTPLP-----PILMAHGKQDMVVPGLAAHQARDSFQKL--GA 174
QY 197 NVTFKTYEGMHSSCOQEMMDVKQFIDKLLP 227
DB 175 TVEYHEY-NMGHEICPDILGLIQSFVKTLP 204

RESULT 15

AB2195
serine esterase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2195
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2195
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <KUR>
A;Cross-references: UNIPROT:Q8YSH2; UNIPARC:UPI00000CE692; GB:BA000019; PIDN:BA074812.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all3113

Query Match 12.5%; Score 151; DB 2; Length 214;
Best Local Similarity 28.4%; Pred. No. 1.5e-06;
Matches 65; Conservative 33; Mismatches 93; Indels 38; Gaps 12;

QY 7 STPLP---AIVPAARKATAA---VIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHA---P 57
DB 6 SXPLSLQFTTVTPAKSQTPAGLVVTLHGWANAEDVASLLPYENLPDYQVFVFNAPVPYP 65
QY 58 VRPVTLMNVAMPWFIDIGLSPDSQED-ESGIKQAEENIK-ALIDQEVKNGIPSNRIIL 115
DB 66 YAPLG-----RSWYDL-----ROENNYEGLAESRELLKDFVLSLSTGTVPLSRTIL 112
QY 116 GGFSGGALSXYTALTTOQKLAGVTALSCWPLRASLPQGPPIGGANRDI-SIQCHGDCD 174
DB 113 SGFSQGGAMTF--DVGSKLPLAGLVVNSGYLHPEALSPD-----NTNIPPTLILHGTRD 164
QY 175 PLVPLMFGSLTVKLTALVNPANVTFTYEGMHSSCOQEMMDV-KQFI 222
DB 165 EVVPLQ---AAVKARTTVESLGVVPVQYQEFEGAGHEINLEMLNVARNFI 209

Search completed: April 13, 2006, 21:18:40
Job time : 43 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 21:10:56 ; Search time 231 Seconds
(without alignments)
702.474 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPAARKA.....CQEMMDVKQFDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1204	99.7	230	1	LYPAL HUMAN	O61608 homo sapien
2	1204	99.7	230	2	O61A01 HUMAN	O61A01 homo sapien
3	1201	99.4	230	2	O5BR77 PONGY	O5BR77 pongo pygma
4	1130	93.5	230	1	LYPAL MOUSE	P97823 mus muscula
5	1130	93.5	230	1	LYPAL_RABIT	O77821 oryctolagus
6	1126	93.2	230	2	O4FK51 MOUSE	O4FK51 mus musculus
7	1125	93.1	230	1	LYPAL RAT	P70470 rattus norv
8	1105	91.5	219	2	O77820 RABIT	O77820 oryctolagus
9	1030	85.3	230	2	O6DJB2_XENTR	O6DJB2 xenopus tro
10	1025	84.9	230	2	O6GR07_XENLA	O6GR07 xenopus lae
11	950	78.6	229	2	O4RN09_TETNG	O4RN09 tetraodon n
12	866.5	71.7	232	2	O6PBW8_BRARE	O6PBW8 brachydanio
13	851	70.4	231	1	LYPAL2 RAT	O9QY18 rattus norv
14	845	70.4	231	1	LYPAL2_MOUSE	O9WT17 mus musculus
15	841	69.6	231	1	LYPAL2_HUMAN	O95372 homo sapien
16	833	69.0	231	2	O6P346_XENTR	O6P346 xenopus tro
17	824	68.2	231	2	O7ZXQ6_XENLA	O7ZXQ6 xenopus lae
18	819.5	67.8	196	2	O568J5_BRARE	O568J5 brachydanio
19	787	65.1	231	2	O9UG00_HUMAN	O9UG00 homo sapien
20	717.5	59.4	236	2	O4SALA4_TETNG	O4SALA4 tetraodon n
21	613.5	50.8	182	2	O5QPQ2_HUMAN	O5QPQ2 homo sapien
22	608.5	50.4	164	2	O5QPQ0_HUMAN	O5QPQ0 homo sapien
23	596	49.3	216	2	O917R0_DROME	O917R0 drosophila
24	592.5	49.0	180	2	O5QPQ3_HUMAN	O5QPQ3 homo sapien
25	558.5	46.2	162	2	O5QPQ1_HUMAN	O5QPQ1 homo sapien
26	552	45.7	215	2	O7PZW9_ANOGA	O7PZW9 anopheles g
27	552	45.7	216	2	O5TKX0_ANOGA	O5TKX0 anopheles g
28	510.5	42.3	223	2	O21224_CAEBL	O21224 caenorhabdi
29	507.5	42.0	239	2	O18501_SCHWA	O18501 schistosoma
30	502.5	41.6	227	2	O9UBF2_SCHJA	O9UBF2 schistosoma
31	495.5	41.0	213	2	O68GW8_CAEBL	O68GW8 caenorhabdi

RESULT 1									
LYPAL HUMAN									
ID	LYPAL HUMAN	STANDARD;							
AC	O75608; O43202; O9UQF9;								
DT	29-MAR-2004 (Rel. 43, Created)								
DT	29-MAR-2004 (Rel. 43, Last sequence update)								
DT	13-SEP-2005 (Rel. 48, Last annotation update)								
DE	Acyl-protein thioesterase 1 (EC 3.1.2.-) (Lysophospholipase I).								
GN	Names=LYPLAI; Synonyms=APT1, LPL1;								
OS	Homo sapiens (Human)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;								
OC	Homo.								
OX	NCBI_TaxID=9606;								
[1]									
RN	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).								
RA	Hu G.;								
RP	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.								
RL									
RN	NUCLEOTIDE SEQUENCE (ISOFORM 1), AND X-RAY CRYSTALLOGRAPHY (1.5								
RP	ANGSTROMS) OF 6-230.								
RC	TISSUE=Testis;								
RX	MEDLINE=20535036; PubMed=11080636; DOI=10.1016/S0969-2126(00)00529-3;								
RA	Devedjiev Y., Dauter Z., Kuznetsov S.R., Jones T.L.Z., Derewenda Z.S.;								
RT	"Crystall structure of the human acyl protein thioesterase I from a								
RL	single X-ray data set to 1.5 A.";								
[3]	Structure 8:1137-1146(2000).								
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).								
RP	TISSUE=Umbilical cord blood;								
RC	MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;								
RA	Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,								
RA	Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,								
RA	Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;								
RT	"Cloning and functional analysis of cDNAs with open reading frames for								
RT	300 previously undefined genes expressed in CD34+ hematopoietic								
RT	stem/progenitor cells.";								
RL	Genome Res. 10:1546-1560(2000).								
[4]									
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).								
RP	TISSUE=Bone marrow, and Eye;								
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,								
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,								
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,								
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,								
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,								
RA	Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,								

32	475	39.3	240	2	O4PID3_USTMA	O4pid3 ustilago ma
33	472	39.1	235	2	O418Q4_GIBZE	O418q4 gibberella
34	469	38.8	245	2	O9HFJ5_NEUCR	O9hfj5 neurospora
35	465	38.5	238	2	O55QW3_CRYNE	O55qw3 cryptococcus
36	465	38.5	238	2	O5KFA4_CRYNE	O5kfa4 cryptococcus
37	459	38.0	244	2	O75QP1_MAGGR	O75qp1 magnaporthe
38	459	38.0	271	2	O51LT0_MAGGR	O51lt0 magnaporthe
39	457	37.8	252	2	O75QP0_MAGGR	O75qp0 magnaporthe
40	456.5	37.8	223	2	O61N31_CAEBR	O61n31 caenorhabdi
41	417.5	34.6	272	2	O6BS88_DEBHA	O6bs88 debaryomyce
42	410.5	34.0	200	2	O83AC9_COXBU	O83ac9 coxiella bu
43	408.5	33.8	239	2	O5ASI2_EMENI	O5asi2 aspergillus
44	400.5	33.2	227	2	O6CGL4_YARLI	O6cgl4 yarrowia li
45	400	33.1	226	2	O54T49_DICDI	O54t49 dictyosteli

ALIGNMENTS

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 127-230 (ISOFORM 1).
RP TISSUE=Brain;
RA Yu W., Sarginson J., Gibbs R.A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Hydrolyzes fatty acids from S-acylated cysteine residues
CC in proteins such as trimeric G alpha proteins or HRAS. Also has
CC low lysophospholipase activity.
CC -!- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
CC protein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O75608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O75608-2; Sequence=VSP_009196;
CC Notes=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: AF081281; AAC31610.1; -; mRNA.
DR EMBL: AF291053; AAG10063.1; -; mRNA.
DR EMBL: AF077198; RAD26993.1; -; mRNA.
DR EMBL: AF077199; RAD26994.1; -; mRNA.
DR EMBL: BC008652; AAH08652.1; -; mRNA.
DR EMBL: BC010397; AAH10397.1; -; mRNA.
DR EMBL: AF035293; AAB88180.1; ALT_INIT; mRNA.
DR PDB: 1FJ2; X-ray; A/B=6-230.
DR OGP: O75608; -;
DR PMMA-2DPAGE; O75608; -;
DR Ensembl: ENSG00000120992; Homo sapiens.
DR HGNC: HGNC:6737; LYPLAL.
DR H-InvDB: HIX007507; -;
DR MIM: 605599; -;
DR GO: GO:004622; F.lysophospholipase activity; TAS.
DR InterPro: IPR003140; PLP_Cestrase.
DR Pfam: PF02230; Abhydrolase_2; 1.
DR 3D-structure; Alternative splicing; Fatty acid metabolism; Hydrolase;
KW Lipid metabolism.
FT ACT_SITE 119 119
FT ACT_SITE 174 174
FT ACT_SITE 208 208
FT VARSPPLIC 57 72 Missing (in isoform 2).
FT
FT CONFLICT 127 131 YTALT -> SLIRG (in Ref. 5).
FT SEQUENCE 230 AA; 24670 MW; 90C0522F765FIAC6 CRC64;
SQ
Query Match 99.7%; Score 1204; DB 1; Length 230;
Best Local Similarity 99.6%; Pred. No. 6e-102;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MCGNNMSTPLPAIIPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIIPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
QY 61 VTLMNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSIYLTALTTOOKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSIYLTALTTOOKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTLPANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTLPANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 2

Q6IAQ1 HUMAN
ID Q6IAQ1 HUMAN PRELIMINARY; PRT; 230 AA.
AC Q6IAQ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LYPLAL protein.
GN Name=LYPLAL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL: CR457103; CAG33384.1; -; mRNA.
DR SMR: Q6IAQ1; 6-229.
DR GO: GO:0003824; P:catalytic activity; IEA.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF02230; Abhydrolase_2; 1.
DR Fatty acid metabolism; Lipid metabolism.
KW SEQUENCE 230 AA; 24670 MW; 90C0522F765FIAC6 CRC64;
SQ

Query Match 99.7%; Score 1204; DB 2; Length 230;

Best Local Similarity 99.6%; Pred. No. 6e-102; Indels 0; Gaps 0; Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIIPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60

DB 1 MCGNNMSTPLPAIIPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

DB 61 VTLMNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSIYLTALTTOOKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180

DB 121 GGALSIYLTALTTOOKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTLPANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

DB 181 FGSLTVEKLTLPANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 3

Q5RBR7 PONPY
ID Q5RBR7 PONPY PRELIMINARY; PRT; 230 AA.
AC Q5RBR7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459O0134.
GN Name=DKFZp459O0134;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OC NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL: CR457103; CAG33384.1; -; mRNA.
DR SMR: Q6IAQ1; 6-229.
DR GO: GO:0003824; P:catalytic activity; IEA.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF02230; Abhydrolase_2; 1.
DR Fatty acid metabolism; Lipid metabolism.
KW SEQUENCE 230 AA; 24670 MW; 90C0522F765FIAC6 CRC64;
SQ

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Cortex;
 RG The German cDNA Consortium;
 RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Ganger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 DR EMBL: CA858568; CH90793.1; -; mRNA.
 DR SMR: OSBR7: 6-229.
 DR GO: GO:0016787; F-hydrolase activity; IEA.
 DR GO: GO:0006631; P-fatty acid metabolism; IEA.
 DR GO: GO:0006629; P-lipid metabolism; IEA.
 DR InterPro: IPR003140; PLP Cesterase.
 DR InterPro: IPR000379; Ser_estr.
 DR Pfam: PF02230; Abhydrolase 2; 1.
 DR Fatty acid metabolism; Hypothetical protein; Lipid metabolism.
 SQ SEQUENCE 230 AA; 24702 MW; E7DC3F90C8AD9997 CRC64;

 Query Match 99.4%; Score 1201; DB 2; Length 230;
 Best Local Similarity 99.1%; Pred. No. 1.1e-101;
 Matches 228; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAFAGIRSHIKYICPHAPVRP 60
 Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAFAGIRSHIKYICPHAPVRP 60

 QY 61 VTLNMNVMPSWFDIIGLSDSDSESGIKQAENIKALIDQSVKNGIPSNRIILGGFSQ 120
 Db 61 VTLNMNVMPSWFDIIGLSDSDSESGIKQAENIKALIDQSVKNGIPSNRIILGGFSQ 120

 QY 121 GGALSYLTATTOQKLAGVTALSCWLPRLASLPQGPFGIGANRRDISILQHGDCDPLVPLM 180
 Db 121 GGALSYLTATTOQKLAGVTALSCWLPRLASLPQGPFGIGANRRDISILQHGDCDPLVPLM 180

 QY 181 FGSLTVEKLTLYNPANVTFTKTEYGMHSSCQEMDMVKQFIDKLLPPID 230
 Db 181 FGSLTVEKLTLYNPANVTFTKTEYGMHSSCQEMDMVKQFIDKLLPPID 230

 RESULT 4
 LYPAL MOUSE
 ID LYPAL MOUSE STANDARD; PRT; 230 AA.
 AC P9783; Q7TPX1; O8BWM6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 1 (EC 3.1.2.-) (lysophospholipase I)
 DE (LysoPLA I) (lysophospholipase I).
 GN Name=Lyplal; Synonyms=Aptl, Plala;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1), PROTEIN SEQUENCE OF 98-105; 150-162
 RP AND 191-201, MUTAGENESIS OF SER-119, AND FUNCTION.
 RC TISSUE=Macrophage;
 RX PubMed=9139730; DOI=10.1074/jbc.272.19.12723;
 RA Wang A., Deems R.A., Dennis E.A.;
 RT "Cloning, expression, and catalytic mechanism of murine
 RT lysophospholipase I";
 RL J. Biol. Chem. 272:12723-12729(1997).
 CC [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
 RC STRAIN=C57BL/6J; TISSUE=Kidney, and Pancreas;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaado I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Fertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Kidney, and Osteoblast;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Skalska U., Smalley D.E.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywiniski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN MUTAGENESIS OF ASP-174 AND HIS-208.
 RP PubMed=9268342; DOI=10.1074/jbc.272.35.22030;
 RX Wang A., Loo R., Chen Z., Dennis E.A.;
 RA "Regiospecificity and catalytic triad of lysophospholipase I";
 RT J. Biol. Chem. 272:22030-22036(1997).
 CC -1- FUNCTION: Hydrolyzes fatty acids from S-acylated cysteine residues
 CC in proteins such as trimeric G alpha proteins or HRAS. Also has
 CC low lysophospholipase activity.
 CC -1- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
 CC protein.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P97823-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P97823-2; Sequence=VSP_009197;
 CC Note=May be due to an intron retention. No experimental
 CC confirmation available;
 CC -1- SIMILARITY: Belongs to the AB hydrolase 2 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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use as long as its content is in no way modified and this statement is not removed.

CC -----
 CC EMBL; U9352; AAB48627.1; -; mRNA.
 CC EMBL; AK002674; BAB22276.1; -; mRNA.
 CC EMBL; AK050549; BAC34318.1; ALT INIT; mRNA.
 CC EMBL; BC013536; AAH13536.1; -; mRNA.
 CC EMBL; BC052848; AAH52848.1; -; mRNA.
 CC HSP; 075608; 1FJ2.
 CC SMR; P97823; 6-229.
 CC ENSMBL; ENSMUSG0000025903; Mus musculus.
 CC MG1; MG1.1344588; Lyp1a1.
 CC GO; GO:0005739; C:mitochondrion; IDA.
 CC InterPro; IPR003140; PLP Cesterase.
 CC InterPro; IPR000379; Ser-estrs.
 CC Pfam; PF02230; Abhydrolase_2; 1.
 CC Alternative splicing; Direct protein sequencing;
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 FT ACT SITE 119 119
 FT ACT SITE 174 174
 FT ACT SITE 208 208
 FT VARSPLIC 214 230
 FT EMBL; U97148; AAC63432.1; -; mRNA.
 FT HSP; 075608; 1FJ2.
 FT SMR; 077821; 6-229.
 FT InterPro; IPR003140; PLP Cesterase.
 FT InterPro; IPR000379; Ser-estrs.
 FT Pfam; PF02230; Abhydrolase_2; 1.
 FT Direct protein sequencing; Fatty acid metabolism; Hydrolase;
 KW Lipid metabolism.
 FT ACT SITE 119 119 By similarity.
 FT ACT SITE 174 174 By similarity.
 FT ACT SITE 208 208 By similarity.
 FT SEQUENCE 230 AA; 24688 MW; 89AF2017AEFC9FAC CRC64;

Query Match 93.5%; Score 1130; DB 1; Length 230;
 Best Local Similarity 91.3%; Pred. No. 3.7e-95;
 Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAI VPAARKATAA VIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 DB 1 MCGNNMSTPLPAI VPAARKATAA VIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 QY 61 VTLLNNVAMPWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLLNNVAMPWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSITYALTITQOKLAGVTALSCWLPPLRASLPQGPICGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSITYALTITQOKLAGVTALSCWLPPLRASLPQGPINSANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTIVNPANVTFTKTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
 DB 181 FGSLTVERLKALINPANVTFTKIYEGNMHSSCOQEMMDVKHFDKLLPPID 230

RESULT 5

LYPAL_RABIT
 ID LYPAL_RABIT STANDARD; PRT; 230 AA.
 AC 077821;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 1 (EC 3.1.2.-) (Lysophospholipase I)
 DE (Calcium-independent phospholipase A2) (CaPLA2).
 DE Names=LyPLA1;
 GN Oryctolagus cuniculus (Rabbit).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OC NCBI_TaxID=9986;
 OX [1]
 RN NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 98-103; 150-161 AND
 RP 191-201.
 RC TISSUE=Kidney;

RX MEDLINE=98308497; PubMed=9644627;
 RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
 RA Sasser M., Cheng J., Buonanno A.;
 RT "cDNA cloning and expression of a novel family of enzymes with
 RT calcium-independent phospholipase A2 and lysophospholipase
 RT activities.";
 RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
 CC -!- FUNCTION: Hydrolizes fatty acids from S-acylated cysteine residues
 CC in proteins such as trimeric G alpha proteins or HRAS. Also has
 CC low lysophospholipase activity (By similarity).
 CC -!- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
 CC protein.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U97148; AAC63432.1; -; mRNA.
 CC HSP; 075608; 1FJ2.
 CC SMR; 077821; 6-229.
 CC InterPro; IPR003140; PLP Cesterase.
 CC InterPro; IPR000379; Ser-estrs.
 CC Pfam; PF02230; Abhydrolase_2; 1.
 CC Direct protein sequencing; Fatty acid metabolism; Hydrolase;
 KW Lipid metabolism.
 FT ACT SITE 119 119 By similarity.
 FT ACT SITE 174 174 By similarity.
 FT ACT SITE 208 208 By similarity.
 FT SEQUENCE 230 AA; 24688 MW; 89AF2017AEFC9FAC CRC64;

Query Match 93.5%; Score 1130; DB 1; Length 230;
 Best Local Similarity 91.3%; Pred. No. 3.7e-95;
 Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAI VPAARKATAA VIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 DB 1 MCGNNMSTPLPAI VPAARKATAA VIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 QY 61 VTLLNNVAMPWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLLNNVAMPWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSITYALTITQOKLAGVTALSCWLPPLRASLPQGPICGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSITYALTITQOKLAGVTALSCWLPPLRASLPQGPINSANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTIVNPANVTFTKTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
 DB 181 FGSLTVERLKALINPANVTFTKIYEGNMHSSCOQEMMDVKHFDKLLPPID 230

RESULT 6

O4FK51_MOUSE
 ID O4FK51_MOUSE PRELIMINARY; PRT; 230 AA.
 AC O4FK51;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Lyp1a1 protein.
 DE Name=Lyp1a1;
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Murioidea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.;

RT "Cloning of mouse full open reading frames in Gateway(R) system entry
RT vector (pDONR201).";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; C7010201; CAJ18409.1; -; mRNA.
SQ SEQUENCE 230 AA; 24689 MW; 0387829D8656BFA2 CRC64;

Query Match 93.2%; Score 1126; DB 2; Length 230;
Best Local Similarity 90.9%; Pred. No. 8.6e-95;
Matches 209; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARAKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARAKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLLNMVAMPSPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMVAMPSPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGANRDISILQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTIVNPAVTFKTYEGMHSSCQEQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTIVNPAVTFKTYEGMHSSCQEQEMDMVKQFIDKLLPPID 230

RESULT 7
ID LYPAL_RAT STANDARD; PRT; 230 AA.
AC P70470;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl-protein thioesterase 1 (EC 3.1.2.-) (lysophospholipase I).
GN Names=Lyplal; Synonyms=Aptl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 20-30 AND 192-196, FUNCTION,
RP AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=96205961; PubMed=8631810; DOI=10.1074/jbc.271.13.7705;
RA Sugimoto H., Hayashi H., Yamashita S.;
RT "Purification, cDNA cloning, and regulation of lysophospholipase from
RT rat liver";
RL J. Biol. Chem. 271:7705-7711(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Hypothalamus;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasser M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with
RT calcium-independent phospholipase A2 and lysophospholipase
RT activities";
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Heart;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PROTEIN SEQUENCE OF 98-112 AND 191-201, AND FUNCTION.
RX PubMed=9624183; DOI=10.1074/jbc.273.25.15830;
RA Duncan J.A., Gilman A.G.;
RT "A cytoplasmic acyl-protein thioesterase that removes palmitate from G
RT protein alpha subunits and p21(RAS).";
RL J. Biol. Chem. 273:15830-15837(1998).
CC -I- FUNCTION: Hydrolyzes fatty acids from S-acylated cysteine residues

CC in proteins such as trimeric G alpha proteins or HRAS. Also has
CC low lysophospholipase activity.
CC -I- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
CC protein.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: Ubiquitous. Detected at low levels in all
CC tissues tested.
CC -I- SIMILARITY: Belongs to the AB hydrolase 2 family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D63885; BAA09935.1; -; mRNA.
DR EMBL; U97146; AAC63430.1; -; mRNA.
DR EMBL; BC085750; AAH85750.1; -; mRNA.
DR HSSP; O75608; 1FJ2.
DR SMR; P70470; 6-229.
DR Ensembl; ENSRNOG00000008320; Rattus norvegicus.
DR GO; GO:0004622; F:lysophospholipase activity; IDA.
DR InterPro; IPR003140; PLP Cesterase.
DR InterPro; IPR000379; Ser-estrs.
DR Pfam; PF02230; Abhydrolase_2; 1.
DR Direct protein sequencing; Fatty acid metabolism; Hydrolase;
KW Lipid metabolism.
FT ACT_SITE 119 119 By similarity.
FT ACT_SITE 174 174 By similarity.
FT ACT_SITE 208 208 By similarity.
SQ SEQUENCE 230 AA; 24709 MW; AAF8C4702EAD74 CRC64;

Query Match 93.1%; Score 1125; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.1e-94;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARAKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARAKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLLNMVAMPSPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMVAMPSPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGANRDISILQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTIVNPAVTFKTYEGMHSSCQEQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTIVNPAVTFKTYEGMHSSCQEQEMDMVKQFIDKLLPPID 230

RESULT 8
ID 077820_RABIT PRELIMINARY; PRT; 219 AA.
AC 077820;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium-independent phospholipase A2 isoform 1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasser M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with

RT calcium-independent phospholipase A2 and lysophospholipase
RT activities.";

RL J. Am. Soc. Nephrol. 9:1178-1186(1998).

DR EMBL; U97147; AAC63431.1; -, mRNA.

DR HSSP; O75608; 1FJ2.

DR SMR; O77820; 1-218.

DR GO; 0003824; F:catalytic activity; IEA.

DR InterPro; IPR003140; PLP Cesterase.

DR InterPro; IPR000379; Ser_estr.

DR Pfam; PF02230; Abhydrolase_2; 1.

FT NON_TER 1

SQ SEQUENCE 219 AA; 23602 MW; 3B6A4FEDC3BC912B CRC64;

Query Match 91.5%; Score 1105; DB 2; Length 219;

Best Local Similarity 96.3%; Pred. No. 6.8e-93;

Matches 211; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 AIVPAARKATAAVIFLHGLDGTGHGWAEPAGIRSHIKYICHPAPVRPVTLLNMVAMPS 71

Db 1 ASVPAARKATAAVIFLHGLDGTGHGWAEPAGIRSHIKYICHPAPVRPVTLLNMVAMPS 60

QY 72 WFDIIGLSPDSQDESGIQAENIKALIDQEVKNGIPSNRIILGGFSGGALSILYALT 131

Db 61 WFDIIGLSPDSQDESGIQAENIKALIDQEVKNGIPSNRIILGGFSGGALSILYALT 120

QY 132 TQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLT 191

Db 121 TQOKLAEVTALSCWLPRLASFPQGPISGANRDISILQCHGDCDPLVPLMFGSLTVEKLT 180

QY 192 LVNPANVTFTYEGMMHSSCQEMDMVKQFIDKLLPPID 230

Db 181 LVNPANVTFTYEGMMHSSCQEMDMVKQFIDKLLPPID 219

RESULT 9

Q6DJB2 XENTR

ID Q6DJB2 XENTR PRELIMINARY; PRT; 230 AA.

AC Q6DJB2

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Lysophospholipase II.

DE Names-lypl2-prov;

GN Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus; Silurana.

OC NCBI_TaxID=8364;

OX [1]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;

RA Klein S., Gerhard D.S.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

DR EMBL; BC075270; AAH75270.1; -, mRNA.

DR SMR; Q6DJB2; 6-229.

DR GO; 0016787; F:hydrolase activity; IEA.

DR GO; 0006631; P:fatty acid metabolism; IEA.

DR GO; 0006629; P:lipid metabolism; IEA.

DR InterPro; IPR003140; PLP Cesterase.

DR InterPro; IPR000379; Ser_estr.

DR Pfam; PF02230; Abhydrolase_2; 1.

KW Fatty acid metabolism; Hydrolase; Lipid metabolism.

SQ SEQUENCE 230 AA; 24510 MW; F12D0BB180E9F89EE CRC64;

Query Match 85.3%; Score 1030; DB 2; Length 230;

Best Local Similarity 80.4%; Pred. No. 5.4e-86;

Matches 185; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

QY 1 MCGNMNSTPLPAIVPAARKATAAVIFLHGLDGTGHGWAEPAGIRSHIKYICHPAPVRP 60

Db 1 MCGNTWSAPLPAIVPAARKATAAVIFLHGLDGTGHGWAEMASIKSPHVKYICHPAPIMP 60

QY 61 VTLNNVAMPSWFDIIGLSPDSQDESGIQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

Db 61 VSLNNMAMPSWFDIIGLSPDAQDEAGIKRAENVKALIDQEKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYALTITQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180

Db 121 GGALSILYALTITQOKLAGVTALSCWLPRLASFPQGPISGANRDISILQCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTLVNPANVTFTYEGMMHSSCQEMDMVKQFIDKLLPPID 230

Db 181 FGTLTSEKLTITISANINFTYSGLMSSCQEMTDIKQFIDKQLPPVN 230

RESULT 10

Q6GP07 XENLA

ID Q6GP07 XENLA PRELIMINARY; PRT; 230 AA.

AC Q6GP07

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MGC80756 protein.

GN Name-MGC80756;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OC NCBI_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RA [2]
 RC NUCLEOTIDE SEQUENCE.
 RX TISSUE=Spleen;
 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 DR EMBL; BC073342; AAH73342.1; -; mRNA.
 DR SMR; Q6GP07; 6-229.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006631; P:fatty acid metabolism; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR003140; PLP_Cesterase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 SQ SEQUENCE 230 AA; 24454 MW; ABE5E723B896DB69 CRC64;

Query Match 84.9%; Score 1025; DB 2; Length 230;
 Best Local Similarity 80.4%; Pred. No. 1.6e-85;
 Matches 185; Conservative 24; Mismatches 21; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
 DB 1 MCGNTWSALPALVPAARKATAAIVFLHGLGDTGHWAEAMASIKSPHVKYICPHAPIMP 60
 QY 61 VTLLNNVAMPSPFDDIIGLSPDSQEDSGIKQAANKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VSLNNMAMPSPFDDIIGLSPDAEDEAGIKKAENVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSYLTALTTOQKLGGVVVALSCWLPRLRSFPQAAANSANKDVAVLQCHGESDPLVPLM 180
 QY 181 FGSITVEKLTIVNPANVTFTYEGNMHSSCOQENMDVKQFIDKLPPI 230
 DB 181 FGFTSEKLTIIISPANVFKTYGLMHSNCOEMTDIKQFIDKLPVNV 230

RESULT 11
 QARN09_TETNG PRELIMINARY; PRT; 229 AA.
 AC QARN09;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 6 SCAF15017, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNAMES=GSTENG00031789001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Betardis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudat V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAE01015017; CAG10223.1; -; Genomic_DNA.
 FT NON_TER 229
 SQ SEQUENCE 229 AA; 24798 MW; 7976729B2D7683AA CRC64;

Query Match 78.6%; Score 950; DB 2; Length 229;
 Best Local Similarity 74.2%; Pred. No. 1.2e-78;
 Matches 170; Conservative 32; Mismatches 27; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
 DB 1 MCGNSMSPALPAIVPAARRATAAIVFLHGLGDTGHSWDTFAGLRUPHVKYICPHAPVMP 60
 QY 61 VTLLNNVAMPSPFDDIIGLSPDSQEDSGIKQAANKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VSLNNMAMPSPFDDIIGLSPDAEDEPGIKQAANKALIDQEVKNGIPSHRIILGGFSQ 120
 QY 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSYLTALTTOQKLAGVVVALSCWLPRLKSPFQASANSANKDLHVLQCHGADPVPV 180
 QY 181 FGSITVEKLTIVNPANVTFTYEGNMHSSCOQENMDVKQFIDKLPPI 229
 DB 181 FGTTAEKMKSLVNPSPHMSFKTYGLCHSACPPEMVDIKRFEKQLPPL 229

RESULT 12
 Q6PBW8_BRARE PRELIMINARY; PRT; 232 AA.
 AC Q6PBW8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein zgc:73210;
 GN ORFNAMES=zgc:73210;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=wild-type; TISSUE=EYE;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wild-type; TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 DR EMBL; BC059556; AAH59556.1; -; mRNA.
 DR HSSP; Q53547; 1AUO.
 DR ZFIN; ZDB-GENE-040426-1715; zgc:73210.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008631; P:fatty acid metabolism; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR003140; PLP Cesterase.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 DR Fatty acid metabolism; Hydrolase; Hypothetical protein;
 KW Lipid metabolism.
 SQ SEQUENCE 232 AA; 25067 MW; 03519A06130EAS50 CRC64;

Query Match 71.7%; Score 866.5; DB 2; Length 232;
 Best Local Similarity 68.5%; Pred. No. 5.3e-71;
 Matches 159; Conservative 28; Mismatches 42; Indels 3; Gaps 1;

QY 1 MCGNNMSTPLP---TVPAAKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAP 57
 DB 1 MCGNNMSTPLPAAEAVTPGTEKETAIVFLHGLGDTGHWADAMTSTIRLPYIKYICPHAP 60
 QY 58 VRPVTLMNVMPSWFDIIGLSPDSQESGSKQAENIKALIDQEVKNGIPSNRIILGG 117
 DB 61 RIPVTLLNKMVWPSFDMGLSPDESPEDEAGIKKRAENIKALIDHEVKNIGIPSNRIILGG 120
 QY 118 FSQGGALSILYALTATTOQKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLV 177
 DB 121 FSQGGALSILYALTATSOQKLAGVGLSCWLPPLHKTFFPQAGASANKTPTILOCHGEMDPMI 180
 QY 178 PLMFGSLTVEKLTLYNPANVTFTKYEYGMHSSCOQEMDMVKQFIDKLLPPI 229
 DB 181 PVQFGATAEKLTIVSPENITFTPTPLGMHSSCPQEMSAVKDFIEKQLPRV 232

RESULT 13
 LYP2 RAT
 ID LYP2 RAT STANDARD; PRT; 231 AA.
 AC Q9QVL8;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II)
 DE (Lysophospholipase 2).
 GN Name=Lyp1a2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugimoto H.;
 RT "Rat lysophospholipase II.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May hydrolyze fatty acids from S-acylated cysteine
 residues in proteins such as trimeric G alpha proteins or HRAS (By

CC similarity). Has lysophospholipase activity (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB021645; BAA87911.1; -; mRNA.
 DR EMBL; BC070503; AAH70503.1; -; mRNA.
 DR HSSP; O75608; 1FJ2.
 DR Ensembl; ENSRNOG00000010067; Rattus norvegicus.
 DR InterPro; IPR003140; PLP Cesterase.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 FT ACT SITE 122 122 By similarity.
 FT ACT SITE 176 176 By similarity.
 FT ACT SITE 210 210 By similarity.
 SQ SEQUENCE 231 AA; 24807 MW; 49A710C5A997C7C1 CRC64;

Query Match 70.4%; Score 851; DB 1; Length 231;
 Best Local Similarity 68.1%; Pred. No. 1.4e-69;
 Matches 158; Conservative 30; Mismatches 40; Indels 4; Gaps 2;

QY 1 MCGNNMSTPL---PAVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAP 57
 DB 1 MCGNNMSTPLLDATAATVSGAERETAIVFLHGLGDTGHWADALSTIRLPYIKYICPHAP 60
 QY 58 VRPVTLMNVMPSWFDIIGLSPDSQESGSKQAENIKALIDQEVKNGIPSNRIILGG 117
 DB 61 RIPVTLLNKMVWPSFDMGLSPDESPEDEAGIKKRAENIKALIDHEVKNIGIPSNRIILGG 120
 QY 118 FSQGGALSILYALTATTOQKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLV 177
 DB 121 FSQGGALSILYALTATCPHPLAGIVALSCWLPPLHRNFPQAANGSA-KDLAILQCHGELDPV 179
 QY 178 PLMFGSLTVEKLTLYNPANVTFTKYEYGMHSSCOQEMDMVKQFIDKLLPPI 229
 DB 180 PVRFGALTAEKLTURVTVPARVQKTPGVNHSSCPQEMAUVKFELEKLLPPV 231

RESULT 14
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 ID LYP2 MOUSE STANDARD; PRT; 231 AA.
 AC Q9WTL7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II)
 DE (Lysophospholipase 2) (Mlyso II).
 GN Name=Lyp1a2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=99165589; PubMed=10064901; DOI=10.1016/S1388-1981(99)00007-4;
 RA Toyoda T., Sugimoto H., Yamashita S.;
 RT "Sequence, expression in Escherichia coli, and characterization of
 lysophospholipase II.";
 RL Biochim. Biophys. Acta 1437:182-193 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Embryo, Kidney, and Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J., Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 RT Nature 420:563-573 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting J., Maman A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: May hydrolyze fatty acids from S-acylated cysteine residues in proteins such as trimeric G alpha proteins or HRAS (By similarity). Has lysophospholipase activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- TISSUE SPECIFICITY: Ubiquitous; detected at low levels.
 CC -1- SIMILARITY: Belongs to the AB hydrolase 2 family.

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 CC EMBL; AB009653; BAA76751.1; -; mRNA.
 CC EMBL; AK003689; BAB22940.1; -; mRNA.
 CC EMBL; AK075590; BAC35841.1; -; mRNA.
 CC EMBL; AK089112; BAC49757.1; -; mRNA.
 CC EMBL; BC068120; AAK68120.1; -; mRNA.
 CC HSP; O75608; 1FJ2.
 CC ENSMUSG00000028670; Mus musculus.
 CC MG1; MG1.1347000; Lypla2.
 CC InterPro; IPR003140; PLP_Cesterase.

DR InterPro; IPR000379; Sex_estrs.
 KW Pfam; PF02310; Abhydrolase_2; 1.
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 FT ACT_SITE 122 122 By similarity.
 FT ACT_SITE 176 176 By similarity.
 FT ACT_SITE 210 210 By similarity.
 SQ SEQUENCE 231 AA; 24794 MW; E18797AL7570AA97 CRC64;
 Query Match 70.0%; Score 845; DB 1; Length 231;
 Best Local Similarity 67.7%; Pred. No. 4.9e-69;
 Matches 157; Conservative 30; Mismatches 41; Indels 4; Gaps 2;
 QY 1 MCGNNMSTPL---PAIVPAARAKATAAVIFLHGLGDTGHGWAEAFAGIRSHIKVICPHAP 57
 DB 1 MCGNTMSVPLLTDAATVSGAERETAAVIFLHGLGDTGHGWADALSTIRLPHVKIICPHAP 60
 QY 58 VRPVTLLNMVAMPSPWFDIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGG 117
 DB 61 RIPVTLLNMVAMPSPWFDLGLSPDAPEDEAGIKKAAENIKALIEHEMKNKGPANRVLGG 120
 QY 118 FSQGGALSLYTALTTOOKLAGVTALSCWLPPLRASLPQGPPIGGANRDISILOCHGDCDPLV 177
 DB 121 FSQGGALSLYTALTCPHPLAGIVALSCWLPPLHRNFPQAAANGSA-KDLAILQCHGELDPMV 179
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RESULT 15
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 ID LYP2 HUMAN STANDARD; PRT; 231 AA.
 AC O95372; Q72422;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II) (LPL-1).
 GN Names=LYPLA2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Testis;
 KU Kuznetsov S.R., Jones T.L.Z.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Yue P., Yu L., Tu Q., Ding J.B., Fu S.N., Zhao S.Y.;
 RT "Cloning and expression of a novel human cDNA homology to murine lysophospholipase I mRNA";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Colon, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: April 13, 2006, 21:18:11 ; Search time 47 Seconds
(without alignments)
404.583 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPAARKA.....CQCEMMVKQFIDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1204	99.7	230	1 US-09-022-940-3	Sequence 3, Appli
2	1204	99.7	230	2 US-09-216-386-3	Sequence 3, Appli
3	1125	93.1	230	1 US-08-844-120-3	Sequence 3, Appli
4	1125	93.1	230	1 US-09-022-940-5	Sequence 5, Appli
5	1125	93.1	230	2 US-09-216-001-3	Sequence 3, Appli
6	1125	93.1	230	2 US-09-216-386-5	Sequence 5, Appli
7	1125	93.1	230	2 US-08-878-862-3	Sequence 3, Appli
8	1125	93.1	230	2 US-09-213-394-3	Sequence 3, Appli
9	1125	93.1	230	1 US-09-988-982-3	Sequence 3, Appli
10	1028	85.1	208	1 US-08-844-120-1	Sequence 1, Appli
11	1028	85.1	208	2 US-09-213-394-1	Sequence 1, Appli
12	1028	85.1	208	2 US-09-988-982-1	Sequence 1, Appli
13	1015	84.0	207	1 US-09-022-940-1	Sequence 1, Appli
14	1015	84.0	207	2 US-09-216-386-1	Sequence 1, Appli
15	841	69.6	231	2 US-09-013-881-7	Sequence 7, Appli
16	841	69.6	231	2 US-09-612-473-7	Sequence 7, Appli
17	644	53.3	176	2 US-09-949-016-9894	Sequence 9894, Ap
18	317.5	26.3	224	2 US-09-540-236-3441	Sequence 3441, Ap
19	296	24.5	242	2 US-09-270-767-46499	Sequence 46499, A
20	279	23.1	218	2 US-09-216-001-4	Sequence 4, Appli
21	279	23.1	218	2 US-08-878-862-4	Sequence 4, Appli
22	275.5	22.8	258	2 US-09-252-991A-20260	Sequence 20260, A
23	275.5	22.8	257	2 US-09-248-796A-16054	Sequence 16054, A
24	274.5	22.7	237	2 US-09-216-001-1	Sequence 1, Appli
25	274.5	22.7	237	2 US-08-878-862-1	Sequence 1, Appli
26	199	16.5	169	2 US-09-599-360B-10	Sequence 10, Appl
27	199	16.5	169	2 US-09-599-360B-111	Sequence 111, App

28	199	16.5	169	2	US-09-513-999C-10	Sequence 10, Appl
29	199	16.5	169	2	US-09-471-276-10	Sequence 10, Appl
30	137.5	11.4	155	2	US-09-902-540-13999	Sequence 13999, A
31	124.5	10.3	243	2	US-09-198-452A-284	Sequence 284, App
32	124.5	10.3	245	2	US-09-438-185A-273	Sequence 273, App
33	117.5	9.7	84	2	US-09-248-796A-16055	Sequence 16055, A
34	115	9.5	246	2	US-09-902-540-14340	Sequence 14340, A
35	101.5	8.4	219	2	US-09-050-739-14	Sequence 14, Appl
36	96.5	8.0	334	2	US-09-902-540-11426	Sequence 11426, A
37	90	7.5	637	2	US-09-328-352-8244	Sequence 8244, Ap
38	88.5	7.3	208	2	US-09-107-532A-6124	Sequence 6124, Ap
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44	88	7.3	1719	1	US-08-459-568-4	Sequence 4, Appli
45	88	7.3	1719	1	US-08-399-411-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-022-940-3
; Sequence 3, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-022-940-3

Query Match 99.7%; Score 1204; DB 1; Length 230;

Best Local Similarity 99.6%; Pred. No. 1.4e-127;

Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLDGTGHGWAEAFAGIRSHSHIKYICPHAVRP 60

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D _b			

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RESULT 2
US-09-216-386-3
; Sequence 3, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-216-386-3

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QY      181  FGSLSATVEKLKTLVNPANVTFKTYEGVMHSSCOEWMMDVKQFIDKLLPPID 233
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      181  FGSLSATVEKLKTLVNPANVTFKTYEGVMHSSCOEWMMDVKQFIDKLLPPID 230
Db      181  FGSLSATVEKLKTLVNPANVTFKTYEGVMHSSCOEWMMDVKQFIDKLLPPID 230

RESULT 3
US-08-844-120-3
; Sequence 3, Application US/08844120
; General Information:
; Patent No. 5858756
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 552244
; JS-08-844-120-3

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RESULT 4
US-09-022-940-5
; Sequence 5, Application US/09022940
: Patent No. 5965423

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/
/
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Shah, Purvi
/ APPLICANT: Murry, Lynn E.
/ TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,940
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 230 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1552244
/ US-09-022-940-5

Query Match 93.1%; Score 1125; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNSAPNPVAVPAARKATAAVIFLHGLGDTGHWAEAFAGIKSHIKYICHPAPVMP 60
QY 61 VTLNMVAMPSPFDIIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLNMSMMPSWFDIIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASFPQGPINSANRDISVLQCHGDCDPLVPLM 180
QY 181 FGSILTVEKLTLPANPVTFKTYEGMHSSCQEQEMMDVKQFIDKLLPPID 230
DB 181 FGSILTVERLKLGNPANVTFKTYEGMHSSCQEQEMMDVKYFIDKLLPPID 230

RESULT 5
US-09-216-001-3
; Sequence 3, Application US/09216001
; Patent No. 604792
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

/
/
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Shah, Purvi
/ APPLICANT: Murry, Lynn E.
/ TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 08/878,862
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0329 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 230 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1552244
/ US-09-216-001-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNSAPNPVAVPAARKATAAVIFLHGLGDTGHWAEAFAGIKSHIKYICHPAPVMP 60
QY 61 VTLNMVAMPSPFDIIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLNMSMMPSWFDIIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOOKLAGVTALSCWLPRLASFPQGPINSANRDISVLQCHGDCDPLVPLM 180
QY 181 FGSILTVEKLTLPANPVTFKTYEGMHSSCQEQEMMDVKQFIDKLLPPID 230
DB 181 FGSILTVERLKLGNPANVTFKTYEGMHSSCQEQEMMDVKYFIDKLLPPID 230

RESULT 6
US-09-216-386-5
; Sequence 5, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```



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;
;
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-216-386-5
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Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSAPMPAVVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVMP 60

QY 61 VTLLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIFSNRIILGGFSQ 120
DB 61 VTLLNMSMPSWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIFSNRIILGGFSQ 120

QY 121 GGALSLYTLTTOQKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTLTTOQKLAGVTALSCWLPRLASFSQGPINSANRDISVLQCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTLPANPVNFKYEGMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLVPANPVNFKYEGMHSSCOQEMMDVKYFIDKLLPPID 230
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RESULT 7
US-08-878-862-3
; Sequence 3, Application US/08878862
; Patent No. 6143544
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,862
```

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;
;
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
;
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0329 US
; TELESCOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1552244
;
US-08-878-862-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSAPMPAVVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVMP 60

QY 61 VTLLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIFSNRIILGGFSQ 120
DB 61 VTLLNMSMPSWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIFSNRIILGGFSQ 120

QY 121 GGALSLYTLTTOQKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTLTTOQKLAGVTALSCWLPRLASFSQGPINSANRDISVLQCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTLPANPVNFKYEGMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLVPANPVNFKYEGMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 8
US-09-213-394-3
; Sequence 3, Application US/09213394
; Patent No. 6319701
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,394
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE:
```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
US-09-213-394-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNMSAPMPAVVPAARKATAAIVFLHGLGDTGHGWAFAFAGIKSSHIIKYICPHAPVMP 60
QY 61 VTLLNMVAMPWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMMMPWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOQKLAGVTALSCWPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOQKLAGVTALSCWPLRASPSQGPINSANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFKYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLGLVNPANVTFKYEGNMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 9
US-09-988-982-3
Sequence 3, Application US/09988982
Patent No. 6838245
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988.982
FILING DATE: 19-No. 6838245-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-988-982-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNMSAPMPAVVPAARKATAAIVFLHGLGDTGHGWAFAFAGIKSSHIIKYICPHAPVMP 60
QY 61 VTLLNMVAMPWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMMMPWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOQKLAGVTALSCWPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOQKLAGVTALSCWPLRASPSQGPINSANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFKYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLGLVNPANVTFKYEGNMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 10
US-08-844-120-1
Sequence 1, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: KIDNNOT19
CLONE: 2676650
US-08-844-120-1
Query Match 85.1%; Score 1028; DB 1; Length 208;
Best Local Similarity 88.7%; Pred. No. 9.4e-108;
Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIKIYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-----PVRP 38
QY 61 VTLLNNVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 39 VTLLNNVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98
QY 121 GGALSILYALTATTOOKLAGVTALSCWPLPLRASIPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 99 GGALSILYALTATTOOKLAGVTALSFLLPLRXSPQGPIGGANRDISILOCHGDCDPLVPLM 158
QY 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCOQEMMDVKQFIDKLLPPID 230
Db 159 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCOQEMMDVKQFIDKLLPPID 208

RESULT 11
US-09-213-394-1

Sequence 1, Application US/09213394
Patent No. 6319701
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,394
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
US-09-213-394-1

Query Match 85.1%; Score 1028; DB 2; Length 208;
Best Local Similarity 88.7%; Pred. No. 9.4e-108;

Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIKIYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-----PVRP 38
QY 61 VTLLNNVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 39 VTLLNNVAMPWFDDIIGLSPDQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98
QY 121 GGALSILYALTATTOOKLAGVTALSCWPLPLRASIPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 99 GGALSILYALTATTOOKLAGVTALSFLLPLRXSPQGPIGGANRDISILOCHGDCDPLVPLM 158
QY 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCOQEMMDVKQFIDKLLPPID 230
Db 159 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCOQEMMDVKQFIDKLLPPID 208

RESULT 12

US-09-988-982-1
Sequence 1, Application US/09988982
Patent No. 6838245
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. 6838245-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-988-982-1

Query Match 85.1%; Score 1028; DB 2; Length 208;
Best Local Similarity 88.7%; Pred. No. 9.4e-108;
Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIKIYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-----PVRP 38

Qy	61	VTLNMNVAMPSWFDIIIGLSPDSQEDESGIKAAENIKALIDQEVKNGIPSNRIILGGFSQ	120
Dd	39	VTLNMNVAMPSWFDIIIGLSPDSQEDESGIKAAENIKALIDQEVKNGIPSNRIILGGFSQ	98
Qy	121	GGALSLYTALTTOQKLAVGTALSCWLPLRASLPQGPICGANRDISILOCHGDCDPLVPLM	180
Dd	99	GGALSLYTALTTOQKLAVGTALSFLLPLRXSFPQGPICGANRDISILOCHGDCDPLVPLM	158
Qy	181	FGSLTVFKLKTLLNPNANVTFTYEGMMHSSCQEQEMMDVKQFIDKLLPPID	230
Dd	159	FGSLTVFKLKTLLNPNANVTFTYEGMMHSSCQEQEMMDVKQFIDKLLPPID	208

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RESULT 13
US-09-022-940-1
; Sequence 1, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-022-940-1

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181 FGSLTVEKLTLLVNPANVTFTKTYEGMHSSCOQEMMDVKQFIDKLLPPI 229
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159 FGSLTVEKLTLLVNPANVTFTKTYEGMHSSCOQEMMDVKQFIDKLLPPI 207
|||||

RESULT 14
US-09-216-386-1
; Sequence 1, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-216-386-1

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RESULT 15
US-09-013-881-7
; Sequence 7, Application US/09013881
; Patent No. 6132964

/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/013,881
/ FILING DATE: HEREMITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BILLINGS, LUCY J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0470 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 231 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: COLANOT02
/ CLONE: 2768301
/ US-09-013-881-7

Query Match 69.6%; Score 841; DB 2; Length 231;
Best Local Similarity 67.2%; Pred. No. 1.5e-86;
Matches 156; Conservative 31; Mismatches 41; Indels 4; Gaps 2;

Qy 1 MCGNNMSTPL---PATVPAARKATAAVIFLHGLDGTGHWAEAFAGIRSHIKYICPHAP 57
Db 1 MCGNTMSVLLTDAATVSGAERETAAVIFLHGLDGTGHSWADALSTIRLPHVKYICPHAP 60

Qy 58 VRPVTLMNVMPSWFDIICLSQDSQESGIKQAAENIKALIDQEVKNGIPSNRIILGG 117
Db 61 RIPVTLLNMKVWPSWFDLMGLSPDAPEDSAGIKKAAENIKALIEHEMKNGIPANRIVLGG 120

Qy 118 FSQGGALSLYLTATTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILQCHGDCDPLV 177
Db 121 FSQGGALSLYLTATCPHPLAGIVALSCLWLPPLHRAFPQAANGSA-KDLAILQCHGELDPWV 179

Qy 178 PLMFGSLTVEKLTLYNPANVTFTYEGMHSSCQEQEMDMVKQFIDKLLPPI 229
Db 180 PVRFGALTAEKLSRVVTPARVQFKTPGVVHSSCQEQEMAAVKEFLEKLLPPV 231

Search completed: April 13, 2006, 21:19:31
Job time : 49 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 21:29:33 ; Search time 167 Seconds
(without alignments)
575.454 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPAARKA.....COQEMMDVKQFDKLLPPIID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pcp:
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pcp:
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pcp:
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pcp:
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pcp:
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1204	99.7	230	4	US-10-236-417-64
2	1204	99.7	263	3	US-09-925-299-991
3	1204	99.7	263	3	US-09-925-299-991
4	1204	99.7	275	5	US-10-450-763-37636
5	1153	95.4	230	4	US-10-210-130-56
6	1153	95.4	230	4	US-10-236-417-60
7	1125	93.1	230	3	US-09-988-982-3
8	1056	87.4	208	4	US-10-131-487A-185
9	1038	85.9	219	4	US-10-106-698-5793
10	1028	85.1	208	3	US-09-988-982-1
11	926	76.7	182	4	US-10-236-417-62
12	841	69.6	231	4	US-10-359-499-7
13	807	66.8	230	4	US-10-237-271-17
14	752	62.3	226	5	US-10-868-577A-66
15	752	62.3	226	5	US-10-868-549-25
16	671	55.5	166	4	US-10-237-271-18
17	671	55.5	166	4	US-10-408-765A-2060
18	644	53.3	146	4	US-10-408-765A-2111
19	596	49.3	216	6	US-11-097-143-28815
20	568	47.1	236	3	US-09-934-392-4
21	510.5	42.3	333	4	US-10-369-493-5135
22	438	36.3	297	4	US-10-369-493-3623
23	381	31.5	89	5	US-10-450-763-37635
24	363.5	30.1	222	4	US-10-369-493-8533
25	356	29.5	227	4	US-10-369-493-22321
26	329.5	27.3	220	4	US-10-369-493-9253
27	326.5	27.0	224	4	US-10-369-493-17607

ALIGNMENTS

RESULT 1

US-10-236-417-64
; Sequence 64, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 64
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-64

Query Match 99.7%; Score 1204; DB 4; Length 230;
Best Local Similarity 99.6%; Pred. No. 1.5e-119;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MCGNNMSTPLPAIVPAARKAATAVIFLHGLDGTGHCMAEAFAGIRSHIKYICPHAPVRP	60
Db	1	MCGNNMSTPLPAIVPAARKAATAVIFLHGLDGTGHCMAEAFAGIRSHIKYICPHAPVRP	60
QY	61	VTLMNVAMPSPWFDIIGLSPDSESGIKQAENIKALIDQVKNGIPSNRIILGGFSQ	120
Db	61	VTLMNVAMPSPWFDIIGLSPDSESGIKQAENIKALIDQVKNGIPSNRIILGGFSQ	120

US-09-925-299-991

Query Match 99.7%; Score 1204; DB 3; Length 263;
Best Local Similarity 99.6%; Pred. No. 1.8e-119;
Matches 229: Conservative 0; Mismatches 1; Indels

Qy	1	MCNNMSTPLPAI	VPAAKATAAVIFL	HGLDGTGHGWA	EAFAGIRSSHIK	YICPHAPVP	60
Db	34	MCNNMSTPLPAI	VPAAKATAAVIFL	HGLDGTGHGWA	EAFAGIRSSHIK	YICPHAPVP	93
Qy	61	VTLNNVAMP	SWFII	GLSPDSEDSGI	KAAENIKALI	DOEVKNGIPSN	IIILGGFSQ 120

Qy	181	FGSLTVEKLTLPANPVTKTYEGMHSSCQEMDVKQFIDKLLPID	230
Qy	214 <th>FGSLTVEKLTLPANPVTKTYEGMHSSCQEMDVKQFIDKLLPID</th> <th>263</th>	FGSLTVEKLTLPANPVTKTYEGMHSSCQEMDVKQFIDKLLPID	263

RESULT 4

US-10-450-763-37636
; Sequence 37636, Application US/10450763
; Publication No. US20050196754A1

1 APPLICANT: Hyseq, Inc
 2
 3 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 4
 5 FILE REFERENCE: 790CIP3/US
 6
 7 CURRENT APPLICATION NUMBER: US/10/450,763
 8
 9 CURRENT FILING DATE: 2003-06-11
 10
 11 PRIOR APPLICATION NUMBER: PCT/US03/08631
 12
 13 PRIOR FILING DATE: 2001-03-30
 14
 15 PRIOR APPLICATION NUMBER: 09/540,217
 16
 17 PRIOR FILING DATE: 2000-03-31
 18
 19 PRIOR APPLICATION NUMBER: 09/649,167
 20
 21 PRIOR FILING DATE: 2000-08-23
 22
 23 NUMBER OF SEQ ID NOS: 60736

Query Match 99.7%; Score 1204; DB 5; Length 275;
Best Local Similarity 99.6%; Pred. No. 1.9e-119;
Matches 229; Conservative 0; Mismatches 1; Indels

Qy	1	MCNNMSTPLPAI	VPAAAKATAA	VTFLHGLDGTGHGWA	EAFAGIRSSSH	KYICPHAPVRP	60
Db	46	MCNNMSTPLPAI	VPAAKATAA	VTFLHGLDGTGHGWA	EAFAGIRSSSH	KYICPHAPVRP	105
Qy	61	VTLNNAVAMP	SWFDIIGLSPDSQ	EDSGIKQAAENI	KALIDQEVKNGI	PSNRILLGFSQ	120
Db	106	VTLNNAVAMP	SWFDIIGLSPDSQ	EDSGIKQAAENI	KALIDQEVKNGI	PSNRILLGFSQ	165
Qy	121	GGALSLYTAL	TTQOKLAGVTAL	SCWLPURASLPQGI	GGANRDISILOCHG	DCDPLVPLM	180
Db	166	GGALSLYTAL	TTQOKLAGVTAL	SCWLPURASFPQGI	GGANRDISILOCHG	DCDPLVPLM	225

RESULT 2

US-09-925-299-991
; Sequence 991, Application US/09925299
; Patent No. US20020055627A1

```

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 991
; LENGTH: 263

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Query Match	99.7%	Score 1204;	DB 3;	Length 263;
Best Local Similarity	99.6%;	Pred. No. 1.8e-119;		
Matches 229:	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy	1	MCNNMSTPLPAIVPAARKATAA	VF	HLGLD	TG	CHWAEAF	FAG	IRSSHI	KYI	CPHAPVRP	60	
Db	34	MCNNMSTPLPAIVPAARKATAA	VF	HLGLD	TG	CHWAEAF	FAG	IRSSHI	KYI	CPHAPVRP	93	
Qy	61	VTLNMMVAMPSNFDI	I	IGL	SPDSQ	DESG	IKAAENIKAL	ID	OEKNGI	PSNRIL	AGFSQ	120

Qy	121 GGALSLYTALTTOOKIAGVTALSCWLPRLASLPQGPIGGANDISIIQCHGDCDPLVPLM 180
Db	154 GGALSIVTAITTOOKIAGVTALSCWLPRLASFPGPIGGANDISIIQCHGDCDPLVPLM 213

	181	FGSLTVEKLTLPNPNVTFKTYEGMHSSCQEMMDVKQFIDKLPPID	230
QY			
	214	FGSLTVEKLTLPNPNVTFKTYEGMHSSCQEMMDVKQFIDKLPPID	263
Dh			

RESULT 3

US-09-925-299-991
; Sequence 991, Application US/099252999
; Publication No. US20030040617A9

```

/ GENNAME: M. GARCIA
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA102
/ CURRENT APPLICATION NUMBER: US/09/925,299
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05883
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 1556
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 991
/ LENGTH: 263
/ TYPE: PRT
/ ORGANISM: Homo sapiens

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QY 181 FGSALTVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230
DB 226 FGSALTVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 275

RESULT 5

US-10-210-130-56
; Sequence 56, Application US/10210130
; Publication No. US20040014053A1

GENERAL INFORMATION:

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Fatturajan, Meera

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Miller, Charles E.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Li, Li

; APPLICANT: Berghs, Constance

; APPLICANT: Zhong, Mei

; APPLICANT: Casman, Stacie J.

; APPLICANT: Voss, Edward Z.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Smithson, Glennda

; APPLICANT: Ji, Weizhen

; APPLICANT: Gorman, Linda

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Leite, Mario W.

; APPLICANT: Guo, Xiaojia Sasha

; APPLICANT: Anderson, David W.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: Ort, Tatiana

; APPLICANT: Ellerman, Karen

; APPLICANT: Rastelli, Luca

; APPLICANT: Agee, Michele L.

; APPLICANT: Chaudhuri, Amitabha

; APPLICANT: Chant, John S.

; APPLICANT: DiPippo, Vincent A.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Eissen, Andrew J.

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Giot, Loic

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Hjalt, Tord

; APPLICANT: Liu, Xiaohong

; APPLICANT: Taupier, Raymond J., Jr.

; APPLICANT: Carterton, Elina

; APPLICANT: Shenoy, Suresh G.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-416C (Cura-716 SMT)

; CURRENT APPLICATION NUMBER: US/10/210,130

; CURRENT FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: 60/309,501

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 60/316,508

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 60/354,655

; PRIOR FILING DATE: 2002-02-05

; PRIOR APPLICATION NUMBER: 60/310,291

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 60/383,887

; PRIOR FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: 60/310,951

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/323,936

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/381,039

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/323,936

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/381,039

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/323,936

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/381,039

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/311,292

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 60/311,979

; PRIOR FILING DATE: 2001-08-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 56

; LENGTH: 230

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-210-130-56

Query Match

Best Local Similarity 95.4%; Score 1153; DB 4; Length 230;

Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHGWAFAFAGIRSSHIIKYICHPAPVRP 60

DB 1 MCGNNMSTPLPTIVPAPRAATTEVFLHGLGDTGHGWAFAFAGIISHHIYICHPAPVRP 60

QY 61 VTILNMNVAMPSWFDIIGLSQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 120

DB 61 VTILNMNVAMPSWFDIIGLSQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSLYALTATTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

DB 121 GGALSLYALTATTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSALTVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230

DB 181 FGSALTVEKLTILVNPANVTFTKTEGMMHSSCOQEMDMVKQFIDKLLPPID 230

RESULT 6

US-10-236-417-60

; Sequence 60, Application US/10236417

; Publication No. US20040048256A1

; GENERAL INFORMATION:

; APPLICANT: Agee et al.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-442C

; CURRENT APPLICATION NUMBER: US/10/236,417

; CURRENT FILING DATE: 2003-01-06

; PRIOR APPLICATION NUMBER: US60/318,120

; PRIOR FILING DATE: 2001-09-01

; PRIOR APPLICATION NUMBER: US60/318,430

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: US60/322,781

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/318,184

; PRIOR FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: US60/361,663

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US60/396,412

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US60/322,636

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/322,817

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/322,816

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/323,519

; PRIOR FILING DATE: 2001-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 341

; SOFTWARE: Custom

; SEQ ID NO 60

; LENGTH: 230

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-236-417-60

Query Match 95.4%; Score 1153; DB 4; Length 230;
Best Local Similarity 94.8%; Pred. No. 4.1e-114;
Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLTIVPAAPRKATTEVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 7
US-09-988-982-3
; Sequence 3, Application US/09988982
; Patent No. US20020081699A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Shah, Purvi
; Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,982
; FILING DATE: 19-No. US20020081699A1-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/213,394
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 552244
; LIBRARY: GenBank
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-988-982-3

Query Match 93.1%; Score 1125; DB 3; Length 230;
Best Local Similarity 91.7%; Pred. No. 4e-111;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 8
US-10-131-487A-185
; Sequence 185, Application US/10131487A
; Publication No. US20040009478A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
; FILE REFERENCE: ALBRE 11
; CURRENT APPLICATION NUMBER: US/10/131,487A
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/623,791A
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/DE99/00721
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 185
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-487A-185

Query Match 87.4%; Score 1056; DB 4; Length 208;
Best Local Similarity 90.0%; Pred. No. 7.9e-104;
Matches 207; Conservative 0; Mismatches 1; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTG-----PVRP 38

QY 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 39 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98

QY 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 99 GGALSLYLTALTTQOKLAGVTALSCWLPRLASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 158

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 159 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 208

RESULT 9
US-10-106-698-5793
; Sequence 5793, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid
; FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 5793
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (43)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5793

Query Match 85.9%; Score 1038; DB 4; Length 219;
Best Local Similarity 89.1%; Pred. No. 7e-102; Mismatches 0; Indels 22; Gaps 1;
Matches 205; Conservative 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 12 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 49
QY 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 50 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 109
QY 121 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 110 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 169
QY 181 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 230
DB 170 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 219

RESULT 10
US-09-988-982-1
Sequence 1, Application US/09988982
Patent No. US20020081699A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Shah, Purvi
Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. US20020081699A1-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-988-982-1

Query Match 85.1%; Score 1028; DB 3; Length 208;
Best Local Similarity 88.7%; Pred. No. 7.6e-101; Mismatches 4; Indels 22; Gaps 1;
Matches 204; Conservative 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 38
QY 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 39 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98
QY 121 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 99 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 158
QY 181 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 230
DB 159 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 208

RESULT 11
US-10-236-417-62
Sequence 62, Application US/10236417
Publication No. US20040048256A1
GENERAL INFORMATION:
APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442C
CURRENT APPLICATION NUMBER: US/10/236,417
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US60/318,120
PRIOR FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: US60/318,430
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US60/322,781
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/318,184
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/361,663
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US60/396,412
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US60/322,636
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/322,817
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/322,816
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/323,519
PRIOR FILING DATE: 2001-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 62
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-62

Query Match          76.7%; Score 926; DB 4; Length 182;
Best Local Similarity 78.7%; Pred. No. 4.7e-90;
Matches 161; Conservative 0; Mismatches 1; Indels 48; Gaps 1;

QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFS- 119

QY 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 120 -----QCHGDCDPLVPLM 132

QY 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCCQEMDMVKQFIDKLLPPID 230
Db 133 FGPLTVEKLTILVNPANVTFTKYEGMMHSSCCQEMDMVKQFIDKLLPPID 182

RESULT 12
US-10-359-499-7
; Sequence 7, Application US/10359499
; Publication No. US20030148363A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/10/359,499
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/612,473
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148363A1 2768301
US-10-359-499-7

Query Match          69.6%; Score 841; DB 4; Length 231;
Best Local Similarity 67.2%; Pred. No. 7.6e-81;
Matches 156; Conservative 31; Mismatches 41; Indels 4; Gaps 2;

QY 1 MCGNNMSTPL---PAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAP 57
Db 1 MCGNTWSVPLLTDAATVSGAERETAIVFLHGLGDTGHGWADALSTIRLPHVKYICPHAP 60

QY 58 VRPVTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 117
Db 61 RIPVTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 120

QY 118 FSQGGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLV 177
Db 117 -----QCHGDCDPLV 132

; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 62
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-237-271-17

Query Match          66.8%; Score 807; DB 4; Length 230;
Best Local Similarity 72.2%; Pred. No. 3.2e-77;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 XXXXXXXXXXXXXFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCCQEMDMVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCCQEMDMVKQFIDKLLPPID 230

RESULT 13
US-10-237-271-17
; Sequence 17, Application US/10237271
; Publication No. US20030096328A1
; GENERAL INFORMATION:
; APPLICANT: THE BURNHAM INSTITUTE
; APPLICANT: SMITH, Jeffrey W.
; APPLICANT: KRIDEL, Steven J.
; APPLICANT: AXELROD, Fumiko T.
; TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS
; FILE REFERENCE: BURN100-1
; CURRENT APPLICATION NUMBER: US/10/237,271
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 60/317,842
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentinh version 3.1
; SEQ ID NO 17
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (35)..(72)
; OTHER INFORMATION: Xaa is any Amino Acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (96)..(120)
; OTHER INFORMATION: Xaa is any Amino Acid
US-10-237-271-17

Query Match          66.8%; Score 807; DB 4; Length 230;
Best Local Similarity 72.2%; Pred. No. 3.2e-77;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 XXXXXXXXXXXXXFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCCQEMDMVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTILVNPANVTFTKYEGMMHSSCCQEMDMVKQFIDKLLPPID 230

RESULT 14
US-10-868-577A-66
; Sequence 66, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
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Job time : 169 secs

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; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-868-577A-66

Query Match      62.3%; Score 752; DB 5; Length 226;
Best Local Similarity 63.9%; Pred. No. 2.3e-71;
Matches 145; Conservative 27; Mismatches 51; Indels 4; Gaps 2;

QY 6 MSTPL---PAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 62
DB 1 MSVPLITDAATVSGARETAIAVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 60

QY 63 LNNVAMPSPFDTIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGG 122
DB 61 LNNKMWNPSPFDTLMLGLSPDAPDEAGIKKAENIKALIEHEMKNKGIIPANRIVLGGFSQGG 120

QY 123 ALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLMEF 182
DB 121 ALSLYTALTCPHLAGIVALSCWLPRLHRAFPQAANGSA-RTWPYSSAMGSWTLPVPRFG 179

QY 183 SLTVEKLTIVNPANTYFTYEGMHSSCCQEMMDVKQFIDKLLPPI 229
DB 180 ALTAELKRSVVTARVQFKTPGVMHSSCPQEMAANKVKEFLEKLLPPV 226
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RESULT 15
US-10-868-549-25
; Sequence 25, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
; FILE REFERENCE: 28967/39117A
; CURRENT APPLICATION NUMBER: US/10/868,549
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,114
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-868-549-25
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Query Match      62.3%; Score 752; DB 5; Length 226;
Best Local Similarity 63.9%; Pred. No. 2.3e-71;
Matches 145; Conservative 27; Mismatches 51; Indels 4; Gaps 2;

QY 6 MSTPL---PAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 62
DB 1 MSVPLITDAATVSGARETAIAVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 60

QY 63 LNNVAMPSPFDTIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGG 122
DB 61 LNNKMWNPSPFDTLMLGLSPDAPDEAGIKKAENIKALIEHEMKNKGIIPANRIVLGGFSQGG 120

QY 123 ALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLMEF 182
DB 121 ALSLYTALTCPHLAGIVALSCWLPRLHRAFPQAANGSA-RTWPYSSAMGSWTLPVPRFG 179

QY 183 SLTVEKLTIVNPANTYFTYEGMHSSCCQEMMDVKQFIDKLLPPI 229
DB 180 ALTAELKRSVVTARVQFKTPGVMHSSCPQEMAANKVKEFLEKLLPPV 226
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Search completed: April 13, 2006, 21:33:11

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OM protein - protein search, using sw model

Run on: April 13, 2006, 21:30:37 ; Search time 27 Seconds
(without alignments)
361.945 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPARKA.....CQEMMDVKQFDKLLPPID 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*
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2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	92	7.6	141	7	US-11-084-508-22
3	87	7.2	338	7	US-11-096-568A-29329
4	87	7.2	346	7	US-11-096-568A-29328
5	87	7.2	353	7	US-11-096-568A-29327
6	87	7.2	397	7	US-11-084-508-5
7	85.5	7.1	373	7	US-11-087-099-4020
8	83.5	6.9	223	7	US-11-096-568A-30586
9	83.5	6.9	279	7	US-11-096-568A-30585
10	83.5	6.9	318	7	US-11-096-568A-30584
11	83	6.9	379	7	US-11-098-686-10741
12	82	6.9	666	7	US-11-072-512-3618
13	82	6.8	616	6	US-10-131-826A-206
14	82	6.8	616	6	US-10-973-115B-206
15	82	6.8	616	6	US-11-290-153-206
16	81	6.7	129	7	US-11-096-568A-12706
17	81	6.7	462	7	US-11-087-099-2138
18	80.5	6.7	462	7	US-11-087-099-5753
19	80.5	6.7	484	7	US-11-188-298-6763
20	80	6.6	299	6	US-10-454-437-228
21	78.5	6.5	631	7	US-11-188-298-3431
22	77.5	6.4	637	7	US-11-079-463-6936
23	77	6.4	256	7	US-11-179-977-2
24	77	6.4	415	7	US-11-079-463-9641
25	77	6.4	481	7	US-11-188-298-3813

26	76.5	6.3	286	7	US-11-079-463-7162	Sequence 7162, Ap
27	76.5	6.3	339	6	US-10-995-076-2	Sequence 2, Appli
28	76.5	6.3	359	7	US-11-098-686-10361	Sequence 10361, A
29	76	6.3	401	7	US-11-096-568A-29666	Sequence 29666, A
30	76	6.3	402	7	US-11-096-568A-29665	Sequence 29665, A
31	76	6.3	520	7	US-11-096-568A-29664	Sequence 29664, A
32	75.5	6.2	269	6	US-10-495-597-14	Sequence 14, Appl
33	75.5	6.2	291	7	US-11-020-602-227	Sequence 227, App
34	75.5	6.2	339	6	US-10-995-076-1	Sequence 1, Appli
35	75.5	6.2	366	7	US-11-087-099-6135	Sequence 6135, Ap
36	75.5	6.2	1972	7	US-11-124-367A-446	Sequence 446, App
37	75	6.2	332	7	US-11-096-568A-19004	Sequence 19004, A
38	75	6.2	441	6	US-10-995-561-638	Sequence 638, App
39	75	6.2	441	6	US-10-995-561-639	Sequence 639, App
40	75	6.2	441	7	US-11-108-519-14	Sequence 14, Appl
41	75	6.2	441	7	US-11-141-554B-14	Sequence 14, Appl
42	74.5	6.2	256	7	US-11-096-568A-20324	Sequence 20324, A
43	74.5	6.2	271	7	US-11-096-568A-20323	Sequence 20323, A
44	74.5	6.2	296	7	US-11-096-568A-20322	Sequence 20322, A
45	74.5	6.2	315	7	US-11-096-568A-12749	Sequence 12749, A

ALIGNMENTS

RESULT 1
US-09-978-360A-443
; Sequence 443, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 443
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -88..-1
US-09-978-360A-443

Query Match 16.5%; Score 199; DB 5; Length 169;
Best Local Similarity 33.8%; Pred. No. 1.6e-12;


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; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 4811687
US-11-096-568A-29327

Query Match
Best Local Similarity 7.2%; Score 87; DB 7; Length 353;
Matches 34; Conservative 20; Mismatches 62; Indels 30; Gaps 6;

QY 19 KATAVIFLHGLGDTGCHGWAEAFAGIRSSHIIKICHPAPVREVTLMNMVAMPSPWFDIIGL 78
Db 24 KEGPVLLHGFDPDLWYWRHQISGLSLGYRAVAP-----DLRGY 64

QY 79 SPDSQDESGIKQAENI-----KALIDQVKNIGPSNRRIILGFSQGGALSALTATQO 134
Db 65 G-DSDSPESFSEYTCINVVGDVLALLDSVAGN---QEKVFLVGHWDGAIIGWFLCLFRPE 120

QY 135 KLAGVTALSCWLPRLASLPQ-GPIGG 159
Db 121 KINGPVCLS--VPYRSRNPVKRPVQG 144

RESULT 6
US-11-084-508-5
; Sequence 5, Application US/11084508
; Publication No. US20050260737A1
; GENERAL INFORMATION:
; APPLICANT: Rahman, Raja Noor Zaliha Abd.
; APPLICANT: Salleh, Abu Bakar
; APPLICANT: Basri, Mahiran
; TITLE OF INVENTION: Novel Lipase Gene from Bacillus sphaericus 205y
; FILE REFERENCE: KAN-101
; CURRENT APPLICATION NUMBER: US/11/084,508
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: MY 20040958
; PRIOR FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Bacillus sphaericus
US-11-084-508-5

Query Match
Best Local Similarity 7.2%; Score 87; DB 7; Length 397;
Matches 63; Conservative 28; Mismatches 82; Indels 108; Gaps 14;

QY 15 PAARKA---TAAVIFLHG---LGDTG--HGWAFAF--AGIRSSHIIKICHPAPVRYPT 62
Db 151 PAKKSGEDVLTPIVQVHGGWVGDKQVQDWNQWMDQGYTFVDQYRMP-----PVA 205

QY 63 LMNMVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQVKNIGPSNRRIILGFSQGG 122
Db 206 -----GWKDEVG--DVKSAIGWIVQHADTYK-----IDPNRIILMGESAGG 244

QY 123 ALSLYTALTTOQKLAGVTALSCWLPRLASLPQGP----- 156
Db 245 NLAMLAAYSLGDK-----HLPSTDPDVPDIKAVINMYGPSDMTAFYKNPNKRVY 295

QY 157 -----IGANRD-----ISILOCH-----GDCDPLVPLMFGSLTVEKLT 191
Db 296 QDVLDQYIGSPSDYPARVKULSPISYIQEHTPTTIFLGTGDIIVPVEQANVLDKLT 355

QY 192 -----LVNPNANVTFTYEGMHSSCCQEMMDVKOFIDK 224
Db 356 SGVAHELXLLPKVDHGHGFANDPGSLSTQFAKE--KVKAFLQK 394
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RESULT 7

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US-11-087-099-4020
; Sequence 4020, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4020
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Methanocaldococcus jannaschii
US-11-087-099-4020
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Query Match
Best Local Similarity 7.1%; Score 85.5; DB 7; Length 373;
Matches 40; Conservative 39; Mismatches 60; Indels 55; Gaps 9;

QY 51 YICHPAPVRPVTLMNMVAMPSPWFDIIGLSPDSQDESGIKQAEN-----IKALIDQEV 104
Db 57 YVINKADLVPKDI-----LEKKEVFG-----ENTVFSAKRLGTKILREMIKQSL 103

QY 105 KN-GIPSNRIILGFSQGGALSALTATTOQK-----LAGVTALSCWLPRLASLPQGP 158
Db 104 KEMGKKEGVGIVGYPNVKSSIIINALTKRKALGTSGVAGLTKEGWVRL----- 153

QY 159 GANRDISILOCHG-----DCDPLVPLMFGSLTVEKLTLVNPA-----NVTFT 202
Db 154 --TKNIKLMDTGVLMEKRDLDV--ISGALREKVENIPPALKILSRINNFDNSIIE 209

QY 203 YEGMHSSCCQEMM 216
Db 210 YFGVDYEEVDELL 223
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RESULT 8

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US-11-096-568A-30586
; Sequence 30586, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30586
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(223)
; OTHER INFORMATION: Ceres Seq. ID no. 4963864
US-11-096-568A-30586
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Query Match
Best Local Similarity 6.9%; Score 83.5; DB 7; Length 223;
Matches 51; Conservative 22; Mismatches 86; Indels 75; Gaps 8;

QY 30 LGDTG-----HGWAFAFAGIRSSHIIKICHPAPVRPVTLMNMVAMPSPWFDIIGLSPDSQ 83
Db 29 IGITGILSGMHAWFAAAADTRYVVVPLIGVQLNKIAATMRPILPCM-----SEY 80

QY 84 EDESGIKQAENI-----KALIDQVKNIGPSNRRIILGFSQGG 122
Db 81 EDGFGFRWAIDENDEWEARVNSIKPLFEARIDLGNKIIDKELVEKY-WNRIAPG----- 133
```

```
QY 123 ALSLYTALTQOKLAGVTALSCWLPRLASLPQGPICGANRDISILQCHGDCDPLVPLMFG 182
Db 134 -----LASKFSPVSLPVIAPRPLYILNGAN-----DPRCPL--G 166

QY 183 SLTV-----EKLKTLVNPANTVFTKTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
Db 167 GLELALKRAEKAYKETASPGNFKFAEDGVGHEATSFMIKESDWDPKFKQED 220

RESULT 9
US-11-096-568A-30585
; Sequence 30585, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30585
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(279)
; OTHER INFORMATION: Ceres Seq. ID no. 4963863
US-11-096-568A-30585

Query Match
Best Local Similarity 6.9%; Score 83.5; DB 7; Length 279;
Matches 51; Conservative 22; Mismatches 86; Indels 75; Gaps 8;

QY 30 LGDTG-----HGWAFAFAGIRSSHIKYICPHAPVRPVTLMNVMAMPWFIDIGLSPDSQ 83
Db 85 IGITISLGGHAWFAAAADTRYVVVPLIGVQLNKIAATMRPILPCN-----SEY 136

QY 84 EDESGIKQAAENI-----KALIDQEVKNGIPSNRIILGGFSQGG 122
Db 137 EDGFGFRWAIDENEWEARNVSIKPLFEARIDLGKNIIDKELVEKV-WNRIAPG----- 189

QY 123 ALSLYTALTQOKLAGVTALSCWLPRLASLPQGPICGANRDISILQCHGDCDPLVPLMFG 182
Db 190 -----LASKFSPVSLPVIAPRPLYILNGAN-----DPRCPL--G 222

QY 183 SLTV-----EKLKTLVNPANTVFTKTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
Db 223 GLELALKRAEKAYKETASPGNFKFAEDGVGHEATSFMIKESDWDPKFKQED 276

RESULT 10
US-11-096-568A-30584
; Sequence 30584, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30584
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(318)
; OTHER INFORMATION: Ceres Seq. ID no. 4963862
US-11-096-568A-30584
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Query Match
Best Local Similarity 6.9%; Score 83.5; DB 7; Length 318;
Matches 51; Conservative 22; Mismatches 86; Indels 75; Gaps 8;

QY 30 LGDTG-----HGWAFAFAGIRSSHIKYICPHAPVRPVTLMNVMAMPWFIDIGLSPDSQ 83
Db 124 IGITISLGGHAWFAAAADTRYVVVPLIGVQLNKIAATMRPILPCN-----SEY 175

QY 84 EDESGIKQAAENI-----KALIDQEVKNGIPSNRIILGGFSQGG 122
Db 176 EDGFGFRWAIDENEWEARNVSIKPLFEARIDLGKNIIDKELVEKV-WNRIAPG----- 228

QY 123 ALSLYTALTQOKLAGVTALSCWLPRLASLPQGPICGANRDISILQCHGDCDPLVPLMFG 182
Db 229 -----LASKFSPVSLPVIAPRPLYILNGAN-----DPRCPL--G 261

QY 183 SLTV-----EKLKTLVNPANTVFTKTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
Db 262 GLELALKRAEKAYKETASPGNFKFAEDGVGHEATSFMIKESDWDPKFKQED 315

RESULT 11
US-11-098-686-10741
; Sequence 10741, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10741
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10741

Query Match
Best Local Similarity 6.9%; Score 83; DB 7; Length 379;
Matches 37; Conservative 20; Mismatches 53; Indels 28; Gaps 6;

QY 12 AIVPA-ARKATAAVIFPLHGLGDTGHGWAFAFAGIRSSHIKYICPHAPVRPVTLMNVMAMP 70
Db 19 AIIPSHASEPIKIGVYPLTGTQNAVGGQLELDGKLAH-----DLNPPVILNRPVQL- 69

QY 71 SWFDIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTAL 130
Db 70 -----FIVDNKSDK---VEAANAVKRLIDQD-----KVCVIIG--SYGSSLSLAGGE 111

QY 131 TTQOKLAGVTALSCWLP 148
Db 112 VAEQAKIPVIGTCTNPL 129

RESULT 12
US-11-072-512-3618
; Sequence 3618, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
```

```

; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3618
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3618

Query Match      6.9%; Score 83; DB 7; Length 666;
Best Local Similarity 18.4%; Pred. No. 4.5; Mismatches 104; Indels 88; Gaps 8;
Matches 51; Conservative 34;

QY 16 AARKATAAVIFL-----HGLGDTGHGWAFAF-----AGIRSSHIIKIC-----53
Db 89 ACKRAAKSLIKLGLERFHGVGILGFNSAEWFTAVGAILLAGLGCYIATNSAEVCQYVI 148
QY 54 -----PHAPVRPVTLLMNVAMP-----SWFDIIGLS---P 80
Db 149 THAKVNILLVENDQQLKILSIPOSSLEPLKAIQVRLPMKNNLYSWDDFMELGRSIP 208
QY 81 DSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSILYALTTOOKLA---137
Db 209 DTQLEQVIESOKANQCAVLIYTSGTGIPKGVML-----SHDNITWIAGAVTKDFKLTDXH 264
QY 138 -----GVTALSCWLPURASLPQGPPIGGANRDISILOCHGDCDPLVPLMFGSLT 185
Db 265 ETVSVYLPPLSHIAAQMMDIWVPIK-----IGALTYFAQADALKGTLVSTLK 310
QY 186 VEKLTALVNPANVTFTKTYEGMHSSCQOQEMDVKQFI 222
Db 311 EVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFV 347

RESULT 13
US-10-131-826A-206
; Sequence 206, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 206
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-206

Query Match      6.8%; Score 82; DB 6; Length 616;
Best Local Similarity 19.4%; Pred. No. 5.1;
Matches 54; Conservative 32; Mismatches 101; Indels 92; Gaps 9;

QY 16 AARKATAAVIFL-----HGLGDTGHGWAFAF-----AGIRSSH-----IKYIC 53
Db 39 ACKRAAKSLIKLGLERFHGVGILGFNSAEWFTAVGAILLAGLGCYIATNSAEVCQYVI 98
QY 54 PHAPVR-----PVTLMNVAMPSPFDIIGLS---79
Db 99 THAKVNILLVENDQQLKILSIPOSSLEPLKAIQVRLPMKNNN--LYSWDDFMELGRS 156
QY 80 -PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSILYALTTOOKLA- 137
Db 157 IPTQLEQVIESOKANQCAVLIYTSGTGIPKGVML-----SHDNITWIAGAVTKDFKLT 212
QY 138 -----GVTALSCWLPURASLPQGPPIGGANRDISILOCHGDCDPLVPLMFGS 183
Db 213 KHETVSVYLPPLSHIAAQMMDIWVPIK-----IGALTYFAQADALKGTLVST 258
QY 184 LTVEKLTALVNPANVTFTKTYEGMHSSCQOQEMDVKQFI 222
Db 259 LKEVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFV 297

RESULT 14
US-10-973-115B-206
; Sequence 206, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
```

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 39870-3330R1C300C1
CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/028,072
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/581,742
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: PCT/US00/05746
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/135,736
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/123,090
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 206
LENGTH: 616
TYPE: PRT
ORGANISM: Homo sapiens
US-10-973-115B-206

Query Match 6.8%; Score 82; DB 6; Length 616;
Best Local Similarity 19.4%; Pred. No. 5.1;
Matches 54; Conservative 32; Mismatches 101; Indels 92; Gaps 9;
QY 16 AARKATAAVIFL-----HGLGDTGHWAEAF-----AGIRSSH-----IKYIC 53
Db 39 ACRKAASLIKGLERFHGVGILGFNSAEWFITAVGAILAGGLCVGIYATNSAEACQYVI 98
QY 54 PHAPVR-----PVTLMNVAMPSPWFDIIGLS-- 79
Db 99 THAKVNILLVENDQLOKILSIPOSSLEPLKALIQVRLPMKNN--LYSWDDFMELGRS 156
QY 80 -PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSXYALTTOOKLA- 137
Db 157 IPTQLEQVIESQKANCQCAVLIYTSGTGIPKGVM-----SHDNITWIAGAVTKDFKLT 212
QY 138 -----GVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLMFGS 183
Db 213 KHETVVSYPPLSHIAAQMMDIWPVK-----IGALTYFAQADALKGTLVST 258
QY 184 LTVEKLTIVNPANVTFTKTEGMMHSSCOQEMDMVKOFI 222
Db 259 LKEVKPTVIGVPOIWEKIHVMYKNSAKSMGLKKKAFV 297

RESULT 15

US-11-290-153-206
Sequence 206, Application US/11290153
Publication No. US20060073568A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C321
CURRENT APPLICATION NUMBER: US/11/290,153
CURRENT FILING DATE: 2005-11-30
PRIOR APPLICATION NUMBER: US/10/146,728
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 206
LENGTH: 616
TYPE: PRT
ORGANISM: Homo Sapien
US-11-290-153-206
Query Match 6.8%; Score 82; DB 7; Length 616;
Best Local Similarity 19.4%; Pred. No. 5.1;
Matches 54; Conservative 32; Mismatches 101; Indels 92; Gaps 9;
QY 16 AARKATAAVIFL-----HGLGDTGHWAEAF-----AGIRSSH-----IKYIC 53
Db 39 ACRKAASLIKGLERFHGVGILGFNSAEWFITAVGAILAGGLCVGIYATNSAEACQYVI 98
QY 54 PHAPVR-----PVTLMNVAMPSPWFDIIGLS-- 79
Db 99 THAKVNILLVENDQLOKILSIPOSSLEPLKALIQVRLPMKNN--LYSWDDFMELGRS 156
QY 80 -PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSXYALTTOOKLA- 137
Db 157 IPTQLEQVIESQKANCQCAVLIYTSGTGIPKGVM-----SHDNITWIAGAVTKDFKLT 212
QY 138 -----GVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLMFGS 183
Db 213 KHETVVSYPPLSHIAAQMMDIWPVK-----IGALTYFAQADALKGTLVST 258
QY 184 LTVEKLTIVNPANVTFTKTEGMMHSSCOQEMDMVKOFI 222
Db 259 LKEVKPTVIGVPOIWEKIHVMYKNSAKSMGLKKKAFV 297

Search completed: April 13, 2006, 21:33:44
Job time : 29 secs